

Result No.	Score	Query Match	Length	DB ID	Description	SUMMARIES
1	1841.5	37.9	934	1	US-08-457-176-2	Sequence 2, Appli
2	1841.5	37.9	934	1	US-08-457-175-2	Sequence 2, Appli
3	1841.5	37.9	934	3	US-08-709-784-1	Sequence 1, Appli
4	1841.5	37.9	934	4	US-09-651-656-3	Sequence 3, Appli
5	1841.5	37.9	934	4	US-09-650-855-3	Sequence 3, Appli
6	1841.5	37.9	934	4	US-09-708-207-13	Sequence 13, Appli
7	1841.5	37.9	934	4	US-09-788-657-19	Sequence 19, Appli
8	1841.5	37.9	1010	4	US-09-512-250C-11	Sequence 31, Appli
9	1818.5	37.4	935	4	US-09-512-250C-33	Sequence 33, Appli
10	1761	36.2	940	4	US-09-512-250C-2	Sequence 2, Appli
11	1571	32.3	1042	4	US-09-512-250C-12	Sequence 32, Appli
12	797	16.4	891	4	US-09-134-9913	Sequence 4913, Ap
13	740.5	15.2	819	4	US-09-651-656-15	Sequence 15, Appli
14	740.5	15.2	819	4	US-09-650-855-15	Sequence 15, Appli
15	724.5	14.9	240	4	US-09-651-656-1	Sequence 1, Appli
16	724.5	14.9	240	4	US-09-650-855-1	Sequence 1, Appli
17	720.5	14.8	858	4	US-09-134-00C-5428	Sequence 5428, Ap
18	719	14.8	885	4	US-09-107-52A-5104	Sequence 5104, Ap
19	715	14.7	855	2	US-08-468-558-2	Sequence 2, Appli
20	715	14.7	855	3	US-08-676-444-2	Sequence 2, Appli
21	708	14.6	1307	4	US-09-252-991A-20867	Sequence 20867, A
22	675.5	13.9	853	2	US-08-468-558-3	Sequence 3, Appli
23	675.5	13.9	853	3	US-08-676-444-3	Sequence 3, Appli
24	663	13.6	874	4	US-09-543-681A-6958	Sequence 6958, Ap
25	654	13.5	855	4	US-09-489-039A-10151	Sequence 10151, A
26	652	13.4	891	4	US-09-328-352-6637	Sequence 6637, Ap
27	646.5	13.3	793	2	US-08-468-558-5	Sequence 5, Appli

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OM protein - protein search, using sw model

Run on: April 7, 2004, 10:41:40 ; Search time 24 Seconds
(without alignments)

2019.866 Million cell updates/sec

Title: US-10-029-065-2

Perfect score: 4859

Sequence: 1 MNENLBEQSKUPELKJDAKQ.....KMKTDLERDAVDHMLQQFF 939

Scoring table: BLOSUM62

Gapext 0.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cn2_6_ptodata/2/iaa/5A_COMB.pep:*

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6: /cn2_6_ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-08-457-176-2
; Sequence 2, Application US/08457176
; Patent No. 5591026

GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert W.
APPLICANT: Kinzler, Kenneth W.
APPLICANT: de la Chappelle, Albert
TITLE OF INVENTION: Mutator Gene and Hereditary
TITLE OF INVENTION: No. 5591026-Polyposis Colorectal Cancer

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie, and Beckett
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/1826-Polyposis Colorectal Cancer
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160295
FILING DATE: 02-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32 141
REFERENCE/DOCKET NUMBER: 01107-44900

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 934 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

US-08-457-176-2

ALIGNMENTS

Query Match Similarity 37.9%; Score 1841.5; DB 1; Length 934;
 Best Local Similarity 43.0%; Pred. No. 1.8e-164;
 Matches 403; Conservative 1/2; Mismatches 307; Indels 55; Gaps 19;

Qy 14 IKLDAKQACQFLSPFKTLKPDP-RAVLFDRDYYTSHGDDATFAETYHTTALRQLG 72
 Db 9 QOLESAEYGFVRFQMPKPTTVRLFRGDPYTAHEGDALAAREYFKTQVICKNG 68

Qy 73 NR-ADALSSYVSXNMFETTARDILLERMDTLELYEGSSN-----WRLVKSGTPGN 124
 Db 69 PAGAKNLQSVLTSKONFESPVKDLILVRYQR-VEVYKNRAGKASKENDYLAYKASPN 127

Qy 125 LGSFEDILFANNEMONSPIAIALAPNGQNCEVGLYDITKRVGLTEFLDDSHFTNL 184
 Db 128 ISQFEDILFGNDMSASIGIVGVRMISAVDQQRQVGIVHVISIQRKLGCEFPDNQFSNL 187

Qy 185 ESALVALGCRCCLYP-AET-GKSSEYRPMFDAISRGCMWYTERKKTTEFKGRDIYQDGLRL 242
 Db 188 EALLIQIGPKCVCPEGETAACDMGKLURQI--IQRGGILITERKKAADFSTKDIYQDNLRL 244

Qy 243 VKG-----SVEPYRDLVSGFECASGALCGCILSYAELADESNTGNYTVKQVNLSNM 294
 Db 245 LKGKIGKGEQMNAAVLPME---NOYAVSSVLAPELLELLSDDSNFQGOFETTEFEFSQYM 300

Qy 295 FLDSAMMRALVHME-SKSDANKNFSLFGLMNRTCTAGMGRKLHLWALKOPLDLYBEBINCR 353
 Db 301 KLDIAVRAVLNLFQGSYEDTTSQSIIALLNK-CKTPQGQNLVNMOKPQMLDKRRIER 359

Qy 354 LDLYCQSFVEDALRDLRCH-LKRSIDIERLTHNLERKRASHLHVVKLYKOSSTRVPTYKS 412
 Db 360 INLVEAFVEDAELRQLTQEDLURRFPLNRAKKFORQAAANLQDCYRLXQGQINQLPNVHQ 419

Qy 413 VLERHDQGPATLIREYDTSLEKWSDNHNLNKFPIGLVETSVDLQDENGYMISSAYDPN 472
 Db 420 ALEXKHGKHOQLLAYVEPTPLDRLSD--FRIKQEMIETTDMDQVENHETLVKPSFDPN 477

Qy 473 ISALKDEQETLERQIRNLHKQTANDLDPKDSLKILDEKTFGHVPOYTRKEEPKVRKQL 532
 Db 478 ISELREIMNDEKRMOSTLISIARDLGDPKQIKLDSRQAFQGYFRVTCKECKVLRN-- 535

Qy 533 NSHYTIVLETRKDGKVETKTYTKUKKLGDOFOQK1VEEYKSCKQRBLARYVQTAASFSEVFAGI 592
 Db 536 NKNFSTVDIQNGKFTNSKQITSLNERYTOKTKEYEAQDAIVKEIWNINSSGYVEMQTL 595

Qy 593 AGVLAEDVLLSFDALAASCPPTPYTRNPISPDGTDLILESCRHPVCAQOWYNSTPNDC 652
 Db 596 NDYLAQDAAVSVFAHNSGAPVTPYVRAILEKGQGRILKASRHACTVEQEDEIAFIPNDV 655

Qy 653 RLVRGYSMFQITGPANGKSTYIIRQGVNTLMAQVSFVPPDNATSIIRDICIARYGAG 712
 Db 656 YFCKDKQMFMHIIITGPNGKSTYIIRQGVVILMAQGCFVPCESEAIVDCILARYGAG 715

Qy 713 DCOLRGVSTFEMOFMLETASILKGATDRSLIITDELGRGSTYDGFGLWAICEHTIVEIK 772
 Db 716 DSOLKGVSTFEMAEMLTASISRSATDSLIIIDELGRGSTYDGFGLWAISEYIATKIG 775

Qy 773 APFLFATHFELTALANKINGDHHKKNAGIAFHVEAHIDPSRKLTMLYKVPHGACDQS 832
 Db 776 AFCMFATHFELTALAN-----QIPTVNNIHTVTAI-TTEETLTMLYQVTKKGVCDQS 825

Qy 833 FGCHVAEPANFPPSVVALAREKASELEDFSPITALIPN-DIKEASKR--KREFDRHDVS 888
 Db 826 FGTHVAELLANPKHVIETAKQKALELEFOYIGESQYDIMEPAAKKCYCYLERE----- 878

Qy 889 RGPARAROFQDPAQLPLDMDPNVVRQKLSKMKTDL 925
 Db 879 QGEKIIQEFPLSKYKOMPFTMSEBENITIKLKQIKAEV 915

RESULT 2
 US-08-157-175-2
 ; Sequence 2, Application US/08457175

Patent No. 5693470
 GENERAL INFORMATION:
 APPLICANT: Vogelstein, Bert
 APPLICANT: Kinzler, Kenneth W.
 APPLICANT: de la Chapelle, Albert
 TITLE OF INVENTION: Mutator Genes and Hereditary
 Tumor Colorectal Cancer
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner, Birch, McKie, and Beckett
 STREET: 1001 G Street, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 SOFTWARE: PatentIn Release #1.0, version #1.25
 APPLICATION NUMBER: US/08/457,175
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/160295
 FILING DATE: 02-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.44900
 TELEPHONE: 202.508.9100
 TELEFAX: 202.508.9299
 TELEX: 197430 BAMB UT
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 934 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-457-175-2

Query Match Similarity 37.9%; Score 1841.5; DB 1; Length 934;
 Best Local Similarity 43.0%; Pred. No. 1.8e-164; Mismatches 307; Indels 55; Gaps 19;

Qy 14 IKLDAKQACQFLSPFKTLKPDP-RAVLFDRDYYTSHGDDATFAETYHTTALRQLG 72
 Db 9 LOLESAAEYGFVRFQMPKPTTVRLFRGDPYTAHEGDALAAREYFKTQVICKNG 68

Qy 125 LGSFEDILFANNEMONSPIAIALAPNGQNCEVGLYDITKRVGLTEFLDDSHFTNL 184
 Db 128 LSQFEDILFGNDMSASIGVYKRSVDPDNQFDSNL 187

Qy 185 ESALVALGCRCCLYP-AET-GKSSEYRPMFDAISRGCMWYTERKKTTEFKGRDLYQDGLRL 242
 Db 188 EALLIQIGPKCVCPEGETAIDMGKLURQI--IQRGGILITERKKADEFSTDYQDNLRL 244

Qy 243 VRG-----SVEPYRDLVSGFECASGALGICLSSVALLADESNVYTVQYINLSYM 294
 Db 245 LKGKIGKGEQMNAAVLPME---NOYAVSSLSAVIPELLELLSDSNFGQFETTDFSQYM 300

Qy 295 RLDSAAMRALNMYE-SKSDANKNFSLFGMLNRCTAGMGRKLHMLKQPLDVERINCR 353

Page 3

Db	716	DSQLRGVSTMAEMIETASLRSATKDSLTIIDEGRGTSTYDGGLAWAISETATKIG	775
Qy	773	APTIPATHFELTALANKNGDNGKKNAGTANPFTYFAHIDPSNRKLTMLXKVHPGACDQS	832
Qy	774	: : : : : : : : : : : : : : : : : :	833
Db	775	AFCMFATHFELTALAN-----QIPTVNNLHYTAL--TTEETLMLYQVKKGCVCDQS	825
Db	823	FGIHVAEFAFPSPVVALAREKASSLEDFPIATPN-DIKEAASRR---KREFFDRHDVS	888
Qy	824	: : : : : : : : : : : : : : : : :	889
Db	825	FGIHVAELANFPKVIECKQKALEEEFOYIGESQGYDIMEPAKKCYLERE-----	878
Qy	879	RGTARAROFQDFQPLDFMDPVNVROKLISKMKDL	925
Db	879	QGEKTIQEFLSKVCOMPFTENSEENITIKQLQKEV	915
RESULT 4			
	US-09-651-656-3		
	Sequence 3 , Application US/09651656		
	Patent No. 6340566		
	GENERAL INFORMATION:		
	APPLICANT: McCUTCHEON-MALONEY, SANDRA		
	APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY		
	TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE		
	POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,		
	TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES		
	FILE REFERENCE: IL-10689		
	CURRENT APPLICATION NUMBER: US/09/651, 656		
	CURRENT FILING DATE: 2000-08-29		
	PRIOR APPLICATION NUMBER: 60/192, 764		
	PRIOR FILING DATE: 2000-03-28		
	NUMBER OF SEQ ID NOS: 106		
	SOFTWARE: Patentin Ver. 2.1		
	SEQ ID NO: 3		
	LENGTH: 934		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
	US-09-651-656-3		
	Query Match	37.9%	Score 1841.5; DB 4; Length 934;
	Best Local Similarity	43.0%	Pred. No. 1.8e-164;
	Matches	403;	Conservative 172; Mismatches 307; Indels 55; Gaps 19;
Qy	14	LKDQKAQGFLSFKTLPKDP-RAVRLPFDRDYTSHGDDATFAETYHTHTLRLQG	72
Db	9	LOLQESAAEYGVPRFFGMPFEKPTTIVRLFRDGFYTAKGEDALLAAREVKTOGTVKMG	68
Qy	73	NR-ADALSSSVSRMFTTARDILLERMDRTLELYEGSGSN-----WRLVSKSTPGN	124
Db	69	PAGKNLQSVLKMRNFESTVKDLVLVRQR-VETYKTRAGNASKENDVLYAASPGN	127
Qy	125	LGSPEDILFANNEMCNSPVTAAALAFNFGONGCEVGLGYDITKRVVGLTBLFDSDHPTNL	184
Db	128	LSQKFEDILFGNNNDMSASIGVGVGKMSAVDQGRQYGVYDSDIQRLGLCBFPDNQFSNL	187
Qy	185	ESALVALGRCRECVP-AET-GKSSEYRPMFDAISRGWVTERKIEFKGRDLVDPDGLRL	242
Db	188	EALLQIGPKCVELGGETADGMGKLRQI--IQRGGLITERKCADSTKDYDNLRL	244
Qy	243	VKG-----SVEPVRDLVSGFECASGAGCILSYAELADESNTYKVNINLSYM	294
Db	245	LKGKGEQMNNSAVLPEME----NOVAVSSLASVIFKELLSDSFQFETTFDSQMY	300
Qy	295	RLDSAMRALNVM-SKSDANKNPFLGCLMNRCTAGMGRLLNMKIKOPLLDVEEINCR	353
Db	301	KLDIARVANLNFLQOSSVEDTGSQSLAALINK-CTCPQGRLVNGWIKOPLMDKRIEER	359
Qy	354	LDLVQSFVEDAALRQDRLRH-LKRSIDERLTHNNEKRSVLVHVKLYOSTRIVYIKS	412
Db	360	LNLYFAVDAELRQDRLQEDLIRRFDLNLAKKKQRQANLQDOCYRLQGINQPNVIIQ	419
Qy	413	VLERHDGOFATLIRRYIDSLEKNSDDNNHLNKFIGLVEVSDPDLENGIMISSAYDPN	472
Db	420	ALERBKGKHQKLLLAFFVTPPTDLSRD--FSKPKQENIETTDMDVQENHBLVKSKSFDPN	477

Qy	473	LSALKDQEETLQRQHNLHKOTANDLDPIDKSLKIDKE TQFGHFRITKKEP KVKQL	532
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Qy	533	NSHYTIVLETRKDG YKFTTYT KLKLGDOFQK1VEEYXSKCOKELVARVQTAASFSEYFAGI	592
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Qy	593	AGVLA ED DYL LS FADLAASC OPT PTY TR PN IS SP DTG D I LE GCR H P CEA QD W NS S LP ND C	652
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Qy	713	DCQLRG V ST M EM L ET A SI L KG A DR S L I IDE L GR G ST D GF G LA W ACE H VE I IK	772
Db	716	DSQ L R G V S TM A EM B ET A TS I RS A K D S L II D E L GR G ST D GF G LA W ACE H Y T KG	775
Qy	773	APT L PA T PH E LT A LN K NG D NG H KK N AG I AN F AY F AH D PS N R K L T ML X K V H P G C D Q S	832
Db	776	AF C MF A TH E LT A LN - -----Q I PT NN L H Y T --T T EET T TM Y Q V K G C D Q S	825
Qy	833	FGIHYA E AF N F P P S T V AL A RA E K A SP L E D F S PI A LL P -DI KA EE A SK R --K R E F DR H D V	888
Db	826	FGIHYA E EL A LN F P K H Y TE C A Q KA L E E F O Y G S Q Y D IM E P A RK C YL E RE-----	878
Qy	889	RGT A AR A RF O LF A Q PL D K D P N V Y R OK L SK M K T D L	925
Db	879	QGEK I QEF L SK V K Y QMP F TEM E EN I TT I KL Q LA E V	915
RESULT 5			
US-09-650-855-3			
	Sequence 3, Application US/09650855		
	Patent No. 636535		
	GENERAL INFORMATION:		
	APPLICANT: MCCUTCHEON-MALONEY, SANDRA		
	APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY		
	TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA		
	TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA		
	TITLE OF INVENTION: MISMATCHES		
	FILE REFERENCE: IL-0284		
	CURRENT APPLICATION NUMBER: US/09/650, 855		
	PRIOR APPLICATION NUMBER: 2000-08-29		
	PRIOR FILING DATE: 2000-08-29		
	NUMBER OF SEQ ID NOS: 106		
	SOFTWARE: PatentIn Ver. 2.1		
	SEQ ID NO 3		
	LENGTH: 934		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
	US -09-650-855-3		
Query Match			
Best Local Similarity 43.0% Pred. No. 1.8e-164; Length 934;			
Qy	Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;		
Db			
Qy	14 LKLD A KQ Q GF S FE T KL P KD P -RAV R FL R RD Y Y T SH G ND A TF A T E T Y H T T A R Q L G	72	
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Qy	73 NR-ADALSSYSVRNM F ET A D I LR D TL E Y G GS S N-----WRLV K SG T PG N	124	
Db	69 PAGAKN L Q S TV L SK M FE S PK D U L V Q Y R -VEV Y KR A G N K A SK N Y L AY K ASP G N	127	
Qy	125 LGSF E D I LF A N M NS O N S PT A LA N F G ONG C GY D IT K RV L GL T EF D LSH F T N	184	
Db	128 LSQ F ED I LF G NN D NS A S I G V G V RM S AV D Q R Q G V G Y D SI Q KL G LC E F P D N Q F S N	187	

RESULT 5
US-09-650-855-3
Sequence 3, Application US/09650855
Patent No. 636555
GENERAL INFORMATION:
APPLICANT: MCCUTCHEON-MALONEY, SANDRA
TITLE OF INVENTION: LAWRENCE LIVERMORE NATIONAL LABORATORY
CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
TITLE OF INVENTION: MISMATCHES
FILE REFERENCE: IL-10284
CURRENT APPLICATION NUMBER: US/09/650,855
CURRENT FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: 2000-08-29
PRIOR FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOs: 106
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 934
TYPE: PRT
ORGANISM: Homo sapiens
US-09-650-855-3
Query Match 37.9%; Score 1841.5; DB 4; Length 934;
Best Local Similarity 43.0%; Pred. No. 1.Bc-164;
Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

RESULT 6		US-09-708-200-13	US Sequence 13, Application US/09708200
		Patent No. 6576468	GENERAL INFORMATION:
		APPLICANT: Nicolaides, Nicholas C	APPLICANT: Niclaides, Nicholas C
		APPLICANT: Grasso, Luigi M	APPLICANT: Grasso, Luigi M
		TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM HYPERMUTABLE CELLS	TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM HYPERMUTABLE CELLS
		FILE REFERENCE: MOR-0005	FILE REFERENCE: MOR-0005
		CURRENT FILING DATE: 2000-11-07	CURRENT FILING DATE: 2000-11-07
		NUMBER OF SEQ ID NOS: 18	NUMBER OF SEQ ID NOS: 18
		SOFTWARE: Patent In Ver. 2.1	SOFTWARE: Patent In Ver. 2.1
		SEQ ID NO 13	SEQ ID NO 13
Dy	185 ESALVALGCRECLVP-AET-GKSSSETRPMDAISRGVMMTERKCKTBFKGRLDVLVDPLGRL 244		
Db	188 EALLIQIGPKCECLVPGGETADGMGKURQI---IQRGGILITERKADEFSTDIYDQLNRL 244		
Dy	243 VRG-----SVEPYRDLVSGFECASGAGCGLSYAELLADESNGNTYKOTVNLSYM 294		
Db	245 LKGKGEQMNNSAVLPEME---NOVAVSSLASAVIKELLELLSDSSNGQFETTFFDSQYM 300		
Dy	295 RLDSRAMRALNTME-SKSDANKNEFLGMLMNRCTAGMKRLLHMMKIKOPLLDVEEINCR 353		
Db	301 KLDIAAVRALNLFGGSVEDDTGSQSSLALLNK-CTPQGQLVNONTIKOPLMDKRIIEER 359		
Dy	354 LDIVQSVTVEDAALRQDILRQH-LKRSIDIERLTHNLRKRAISLHVWVKKLYQSSTRPVYIKS 412		
Db	360 IMLVNEAVEPDAELRQTIQEDLJLRRFPDLNRLAKKFQDQAANLQDCPRLYQINGOLPNVIQ 419		
Dy	413 VLERHDQFQFATLIREYRVIDSLPEKWSDDONHNLKXPIGLVETSYDLDQLENGEMYISSAYDPN 472		
Db	420 ALEXHEGKHQKILLAAVFTPLTLRSR -FSKQEMIETTLDMDQENHETLVKSFDPN 477		
Dy	473 LSALKDQEETLEROIHNHLKQTANDLDPIDKSLKLKDKETOFGHVFRTKKEEPKVKRQL 532		
Db	478 LSELREIMNDLKEKMQSTLISAAARDLQDGPQIKLDSAQGYFRVTCBKEKYLRLRN-- 535		
Dy	533 NSHYIVLETRDKGVKFETYKTKLKGIDOFQKVVEYKSQKELVARVUQTAASFSESTYFAGI 592		
Db	536 NKGNTVSDIOKNGKVFNTSKLTSLNNEBYTNKNTTEYEEAQDALVKEVNUISSGGYVPMQTL 595		
Dy	593 AGTYLAEDVLSPADAASCPTPYTRPNISPDTGDLILEGRHPCPCEAQDWNVS1PNDC 652		
Db	596 NDYLAQDAVSVFAHVENGAPVYWRPAILEKGQGRILKASRHADEVQDEIAFPNDV 655		
Dy	653 RLYRGESWFOILTGPNGGGKSTYIROYGVNTLMAQGFSVPCDNATISIRDCAFARYGAG 712		
Db	656 YFEKDQMFHITGPNGGGKSTYIQRGVIVMAQGFCVPCEAESIVDCLLARVGAG 715		
Dy	713 DCQLRGSYSTEMQEMLEPASTLKGATDSLIIIDELGRGTSTYDGFGHAWAICEHTVEIK 772		
Db	716 DSDLGKGVSTMEMLEPASTIRSATDSLIIIDELGRGTSTYDGFGHAWAISEYATKIG 775		
Dy	773 APTIFATHFELHTALANKNGDNGHKKNAGIANFHVFHIDPSNRKUTMLYKVPHGACDQS 832		
Db	776 AFCMFATHFELHTALAN-----Q1P7VNNLHVHTL-TTEETLTMLYQVKKGVCQDS 825		
Dy	833 FGTHVAEFNPBPSSVALAREKASELEDFSPIAIIPN-DIKEAASKR--KREFDRHDVS 888		
Db	826 FGTHVAELANFPKXIECAKQKALEELEYFOYIGESQGYDIMEPAKKCYLERE----- 878		
Dy	889 RGTAARAROFQDPAQLPDKMDENVYQKLSSRMKTDL 925		
Db	879 QGEKIIQEFLSKYXQMPFTEMSEBNITIKLKOLKAEV 915		

RESULT 6
US-09-708-200-13
; Sequence 13, Application US/09708200
; Patent No. 6576468
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi M
; APPLICANT: Sass, Philip M
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
; TITLE OF INVENTION: HYPERMUTABLE CELLS
; FILE REFERENCE: MOR-0005
; CURRENT APPLICATION NUMBER: US/09/708,200
; CURRENT FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13

Patent No. 6656736
 GENERAL INFORMATION:
 APPLICANT: Nicolaides, Nicholas
 SASS, Philip
 APPLICANT: Kinzler, Kenneth
 APPLICANT: Grasso, Luigi
 APPLICANT: Vogelstein, Bert
 TITLE OF INVENTION: Methods for generating hypermutable
 TITLE OR INVENTION: Yeast
 FILE REFERENCE: 01107-0097
 CURRENT APPLICATION NUMBER: US/09/788,657
 PRIORITY DATE: 2001-02-21
 PRIOR APPLICATION NUMBER: 60/184,336
 PRIOR FILING DATE: 2000-02-23
 SEQ ID NO: 25
 SOFTWARE: FastSEQ for Windows Version 3.0
 LENGTH: 934
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-788-657-19

Query Match Score 37.9%; Score 1841.5; DB 4; Length 934;
 Best Local Similarity 43.0%; Pred. No. 1.8e-164;
 Matches 403; Conservative 172; Mismatches 307; Indels 5; Gaps 19;

Qy 14 IUKLDAKQAQGFLSFFKTLPPKDP-RAVRLFORDYYTTSHGDDATTAETYHTTTALRQG 72
 Db 9 IQLLESAEVGVVRFFGMPPEPPTVRLFDGDFTRAGEBAAAREYFTQGVLYKM 68
 Qy 73 NR-ADALSSVSYSRMNPETTARDILLERMORTTLEYEGSSN----WRLVKGSTPGN 124
 Db 69 PAGAKNQSYVTSKUNFESFKYDILLYROTE-VEYKNRACKNSKENDTLYAKASPGN 127
 Qy 125 IGSFEDLFANEMONSVPIALAPNEGQNCEVGlyVDITKRVGLTEPLDOSHFTNL 184
 Db 128 ISQFEDLFGNNDMSAISIGTVGKMSAVIDGGRQVGYDVSIDQRKGICLCEFPDNQFSNL 187
 Qy 185 ESALVALGCRECLVP-AET-GKSSEYRPMPDAISRGVMMTERKETEFKGRLYODLGRL 242
 Db 188 EALLIQGPBKPVLPGETTAGDMGKURQI---IQRGILITERKAADFSTDYQDNLRL 244
 Qy 243 VKG-----SVEPYRDLVSGFECASGALGCGILSYAELADESNYGNNTVKOYNNSM 294
 Db 245 IKGKKGKQMNNAVLPME---NOVAVSSLASAVIKLELSDDSNFGOFFLTTFPSOM 300
 Qy 295 RLDSAMRALTME-SKSDANKNFSFGLMNRCTAGMGRLLMNLKQPLDVEBINC 353
 Db 301 KLDIAAVRNALNLFQGSVEDTGSOSLAALINK-CXTPQGFLVNWQIKOPMDKRIBER 359
 Qy 354 IJLVQSVFEDALRQDLRQH-LKRSIDIERLTHNLBRKASLVHVVKLYQSTRVPIKS 412
 Db 360 IMLVEAFVEDAELRQDRLQEDILRFDLNLAALKPQRCAANLQDCRYLQGINLENVIQ 419
 Qy 413 VLERHDQGOFATLIREYITDLSLEWKSDDNHLNKFIGLVEYSTDLDOLENGEMISSAYDPN 472
 Db 420 ALEKHEKGKHQKULLAVLAVTPYLDRSLD-FSKPQENILETTDMDQVNHELVKSFDPN 477
 Qy 473 LSAIKDEQETLERQHNLHKQTANDLPIDKSLKLKDKEQFHYRITKKEEPVKRQL 532
 Db 478 LSELREIMNDLEKMKOETLISAAARDGLDPERQKIKLSSAQFGYZXERVTCCEKVLRN-- 535
 Qy 533 NSHYVILETRQGKFTYTKLKGDOFQKVEYKSCQRELVARYVQTANSFSEVPGI 592
 Db 536 NKNFSTDYDQNGVKFTNSKLTSLNEBYTKTKEYEAQDAIVKEIWNISGGYEPMTL 595
 Qy 593 AGYLAELDVLULSFAADLAASCPTPYTRNISPDTGDTILEGCRHPCEVAQDWNSIPNDC 652
 Db 596 NDVLQDAVSVTAHVNGAPVYVRAILEKGQTRILKASRHAEVQDIAFIPNDV 655
 Qy 653 RLVRGESWFOQIITGPNGGKSTYIROYGNTYIIMAQGWSFVPCDNATISIRRCIFARVAG 712
 Db 656 YFEKDKDMFHITGPNGGKSTYIROYGVTIIMAQGCFVPCESAEVSVICILARVGRG 715

RESULT 8
 US-09-512-250C-31
 Sequence 31, Application US/09512250C
 Patent No. 65180422
 GENERAL INFORMATION:
 APPLICANT: Borcher, Torben
 APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis
 APPLICANT: Vind, Jesper
 TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells Used in the Mismatched Repair System
 TITLE OF INVENTION: No. 65180421 Cloned Gene Involved in the Mismatched Repair System
 TITLE OF INVENTION: Cell 1B
 FILE REFERENCE: 5718-200-US
 CURRENT APPLICATION NUMBER: US/09/512,250C
 CURRENT FILING DATE: 1999-02-24
 NUMBER OF SEQ ID NOS: 33
 SEQ ID NO: 31
 LENGTH: 1010
 TYPE: PRT
 ORGANISM: human_P
 US-09-512-250C-31

Query Match Score 37.9%; Score 1841.5; DB 4; Length 1010;
 Best Local Similarity 43.0%; Pred. No. 2.1e-164;
 Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

Qy 14 IKLDAKQAQGFLSFFKTLPPKDP-RAVRLFDRDYTTSHGDDATTAETYHTTTALRQG 72
 Db 85 IQLLESAEVGVVRFFGMPPEPPTVRLFDGDFTRAGEBAAAREYFTQGVLYKM 144
 Qy 73 NR-ADALSSVSYSRMNPETTARDILLERMORTTLEYEGSSN----WRLVKGSTPGN 124
 Db 145 PAGAKNQSYVTSKUNFESFKYDILLYROTE-VEYKNRACKNSKENDTLYAKASPGN 203
 Qy 125 IGSFEDLFANEMONSVPIALAPNEGQNCEVGlyVDITKRVGLTEPLDOSHFTNL 184
 Db 204 LSQFEDLFGNNDMSAISIGTVGKMSAVIDGGRQVGYDVSIDQRKGICLCEFPDNQFSNL 263
 Qy 185 ESALVALGCRECLVP-AET-GKSSEYRPMPDAISRGVMMTERKETEFKGRLYODLGRL 242
 Db 204 EALLIQGPBKPVLPGETTAGDMGKURQI---IQRGILITERKAADFSTDYQDNLRL 320
 Qy 243 VKG-----SVEPYRDLVSGFECASGALGCGILSYAELADESNYGNNTVKOYNNSM 294
 Db 321 LKGKKGQBMNSAIPME---NOVAVSSLASAVIKPLELLSDDSNFGOFFLTTFPSOM 376
 Qy 295 RLDSAMRALTME-SKSDANKNFSFGLMNRCTAGMGRLLMNLKQPLDVEBINC 353
 Db 377 KLDIAAVRNALNLFQGSVEDTGSQSLAALINK-CXTPQGFLVNWQIKOPMDKRIBER 435
 Qy 354 LDLVQSVFEDALRQDRLQEDILRFDLNLAALKPQRCAANLQDCRYLQGINLENVIQ 436
 Db 436 IMLVEAFVEDAELRQDRLQEDILRFDLNLAALKPQRCAANLQDCRYLQGINLENVIQ 495
 Qy 443 VLERHDQGOFATLIREYITDLSLEWKSDDNHLNKFIGLVEYSTDLDOLENGEMISSAYDPN 472

496 ALEXHEGEHQKQLLAVFTPLTDLRSD--FSKQEMIERTLMDQVNEBFVLPKFSDEN 553
 473 LSAKDEQETLERQHNLHKQTANDLPIDKSKLKDKEFGEVERTRIKEEPEVKRQL 532
 554 LSEIREIMDLEKRQHNMOSTLISAARDGLGDKQIKLSSAQFGTYFRVCKEEVKYLN-- 611
 533 NSHYIVLTERKDKGYFTYKLKKLQDFOKIVEEKYSCOKELVAVVQTAASREVFGI 592
 612 NKNFESTVDILOKNGKFTNSKLTSLNEEYTKNKTKEYEAQDAIVKEVNISGIVYEPMQTL 671
 593 AGVIAEDLVLSFDLAASCPPTPYTRPNISPDTGDIILEGRHCPCEAODWYNSIPNDC 652
 672 NDVLAQDAAVSFAHVNSGAPVPTVRPALEKGQRIILKASeHACVEQDEIAFIPNDV 731
 713 DCOLRGVSPTEPMQMLETASILKGTATDRSIIIDBLGRGSTYDSEGLAWAICEHIVEIK 772
 792 DSQLGKVSPTEMAEMLETASILRSATKDSLIIIDBLGRGSTYDSEGLAWAISEYIATKIG 851
 773 APTIFATHPHETLALANRQNGDNGHHRKNAGIANFNFVAHTDPSNRKLTMLYKWHFGACDQS 832
 852 AFCMFATHPHETLALAN-----QIPTYNNLHTAL-TTEBTLMYLQVKKGVCQDS 901
 833 FGIVAAEFANFPSPSYVALAREKAELDEDSPITALPN-DIKEAKASKR---KRFEDRHVS 886
 902 FGIVAAELANPARKHVICAKQKALEEQQYIGSQGTDIMEPAKCYLRE----- 954
 889 RGTARAROFIQDFAQLPDKMDPNNVVRQKLSKMKTDL 925
 955 QGEKLIQEFLSKVQMPFTEMSEENITIKLKQKRAEV 991

RESULT 9
 US-09-512-250C-33
 ; Sequence 33, Application US/09512250C
 ; Paten No. 6518042
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben
 ; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis
 ; APPLICANT: Vind, Jasper
 ; TITLE OF INVENTION: A Process for Making DNA Libraries In Filamentous Fungal Cells
 ; TITLE OF INVENTION: No. 6518042el Cloned Gene Involved in the Mismatched Repair System
 ; TITLE OF INVENTION: Cells
 ; FILE REFERENCE: 5718-200-US
 ; CURRENT APPLICATION NUMBER: US/09/512,250C
 ; NUMBER OF SEQ ID NOS: 33
 ; SEQ ID NO: 33
 ; LENGTH: 935
 ; TYPE: PRT
 ; ORGANISM: mus. P.
 US-09-512-250C-33

Query Match Score 1818.5; DB 4; Length 935;
 Best Local Similarity 44.3%; Pred. No. 2.7e-162;
 Matches 395; Conservative 173; Mismatches 318; Indels 47; Gaps 18;

QY 14 IKLDAKQACQFLSPFKTLPKDP-RAVRLDRDYTSHGDDATIAETYYHHTALRQG '72
 Db 9 LQLEGAEGAFVRFEGMPEKPKSTVRLFDRGDEYTAHGEDALLAAREVFTQGVKYM '68
 Qy 73 NR-ADALPSSVSRNMETTAFALPNTGQNGCEVGLYWDITKRVGLTEFLDDSHFTNL '124
 Db 69 PAGSKTLQSYULSKMFNFSEVKDILLVRQR-VEVYKAGKASKENEWYLAFKASQN '227
 Qy 125 LGSFEDILFANNEWCONSPVIALAPNFGONGCEVGLYWDITKRVGLTEFLDDSHFTNL '184
 Db 128 LSQFEDILFENNDMSASVGMGIRMAVWDQRRHVGTVYSTORKLGCLCEPPENDQFSNL '187

185 ESALVALGGCRECLYPA--ETGKSSEYRPMFDAISRCGYMVTERKTTFGRDLVQDLGRL 242
 Db 188 EALIJIQGKECVLPGGETGDMGKLRL--QVIQRGGLITERKADSTKDIYDQDLRL 244
 Qy 243 VKGSV-EPYRDLV--SGFECASGALGCCILSYABLADESNYGNVTYKQYNLSYMRUDS 298
 Db 245 LKGKGEQINSAALPEMNQVAVSSLAVTIKFELLLSDSNGFOELATEDFSQYKLDM 304
 Qy 299 AMBALNVM--SKSDANKNSLFCUMLNTCTAGNGKRLHMMKQPLDVEEINCRDLY 357
 Db 305 AAVALNLFQGSVSEBDTGQSLSALLNKC-CKTAGQQRVLNQVWIKOPUMDRNRLBEERLVY 363
 Qy 358 QSFVEDAALRQDH-LKRSIDLERLTINLERKASLHVHVVLYQSTRPVYIKSVLER 416
 Db 364 EAFYEDSERQSLQEDIJLRFPDLNRLAKKFQROAANLQDCYRQYQGINQNLPSVIALEK 423
 Qy 417 HDGQFATLIRYRIDSLSKFWSDDNHNLNPKLFIGLYETSVQDLENGEYMISSAYDPNLSA 476
 Db 424 YEGRHQAQLLAVFTPLDLRSR -FSKQEMIETTLDQDQVENEHEFLVKPFSFDPLNSEL 481
 Qy 477 KDEQEFLERQHNLHKQTAANDLPIPDLSKLKDKEFGEVERTRIKEBPKVQKLNQHRY 536
 Db 482 REYDGLEXRKMQSTLINAARGLGLDGPQKOKSSAQGYYFRTCKEKEVLRN-NKMF 539
 Qy 537 IVLETRKDGKFTYTKLKGQFQKIVEEYKSKQEEVYARVYOTAASEVFAGIYGT 596
 Db 540 STVDIQKNCVKFTNSELSSLNEETYKNGEYEEAQDAIVKEIUNISSGYEPHOTINDYL 599
 Qy 597 AEIDVLLSPADLAASCPPTPYTRPNISPDTGDLIEGCRHPCYEAODVYNSIPNDCRUVR 656
 Db 600 AHLDAAIVSPAHVNSNAAPYFVPRVPLKGRKGRILLKASHACVEQDEVAFIPNDVHEK 659
 Qy 657 GESWFQITGPNGKGSKTYIROGVNVYMAQVSFVPCTDNATISIRDCLFARYGAGDQQL 716
 Db 660 DKQMFEPHITGPNGKGSKTYIQTQTCVIMAQGCFVPCEASVIVDCILARYGAGDQQL 719
 Qy 717 RGYSTFMQEMLEPASILKGTATDRSIIIDBLGRGSTYDSEGLAWAICEHIVEIKPTL 776
 Db 720 KGYSTFMQEMLEPSSILRSATKDSLIIIDBLGRGSTYDSEGLAWAICEHIVEIKPTL 779
 Qy 777 FATHFELTALANRQNGDNGHHRKNAGIANFHFVAHTDPSNRKLTMLYKTHPGACDQSGFH 836
 Db 780 FATHFELTALAN-----QIPTVNNLHTAL-TTEBTLMYLQVKGVCDQSGFH 829
 Qy 837 VAEPANFPESYVALAREKAELDEDSPITALPN-DIKEAKASKR---REFDRDHSVSRGTA 892
 Db 830 VAELANFPRHVIACAKOALLEBEFQNGTSLGCDDEAPAAKERCLERE-----QCEK 882
 Qy 893 RAROFLOQAQLPDKMDPNNVVRQKLSKMKTDL 925
 Db 883 TLEFLSSKVQVPEFTAMSEESISAKLKQKLAEV 915

RESULT 10
 US-09-512-250C-2
 ; Sequence 2, Application US/09512250C
 ; Patent No. 6518042
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben
 ; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis
 ; APPLICANT: Vind, Jasper
 ; TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells US-
 ; TITLE OF INVENTION: Cells
 ; FILE REFERENCE: 5718-200-US
 ; CURRENT FILING DATE: 1999-02-24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 33
 ; LENGTH: 935
 ; TYPE: PRT
 ; ORGANISM: mus. P.
 US-09-512-250C-2
 ; Sequence 2, Application US/09512250C
 ; Patent No. 6518042
 ; GENERAL INFORMATION:
 ; APPLICANT: Borchert, Torben
 ; APPLICANT: Pedersen (Executor for Lars Christiansen, deceased), Dennis
 ; APPLICANT: Vind, Jasper
 ; TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells US-
 ; FILE REFERENCE: 5718-200-US
 ; CURRENT FILING DATE: 1999-02-24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 2
 ; LENGTH: 940
 ; TYPE: PRT

ORGANISM: *Aspergillus oryzae*
US-09-512-250C-2

Db 939 AL 940

Query Match Score 1761; Length 940;	DB 4;	Length 11.
Best Local Similarity 41.7%; Pred. No. 7.5-157;	DB 5;	Sequence 32, Application US/09512250C
Matches 401; Conservative 173; Mismatches 316; Indels 72; Gaps 25;	DB 6;	Patent No. 6518042
Qy 9 SKUPELKIDAKOAGGLFDRDDYTSHGDDATFLAFTYYHPTT 66	DB 7;	GENERAL INFORMATION:
Db 2 SSRPLKVD--DEVGFIRYRSLANSNDETIRFDGFWYIARGAKAFIARTVYKTT 59	DB 8;	APPLICANT: Pedersen, Torben
Qy 67 ALRQLGNRADA--LSSSVSRSRNMFTIARDILLERMDRTLELYEGSGS --NWRVKSGT 121	DB 9;	APPLICANT: Vind, Jesper
Db 60 IRLRNG-RSDGGFLPSVMSVTVERNLFREALF-RLNKRKIEINGSVGTRKGHWKLKOAS 117	DB 10;	TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells Used in the Mismatched Repair System
Qy 122 PGNLGSFEDIL--PANNEMQNSPVTAALPNFGNGCE --YGLGYDITKRVGLIGTEFL 176	DB 11;	TITLE OF INVENTION: A process for Making DNA Libraries In Filamentous Fungal Cells Involved in the Mismatched Repair System
Db 118 PGN1QDVDEEGLSYGGLSMWDSAPTI--LAVKISAKAAEARSYRGVSEFL 175	DB 12;	NUMBER OF SEQ ID NOS: 33
Qy 177 DDSHFTNLESALVALGCRELVPAAFTGKSEYRPMEDALS-RGCGVMVTRKCTBFGKDL 235	DB 13;	SOFTWARE: PatentIn version 3.1
Db 176 NDITYSNFSLLIIQGVKECLVQMDANKCVELGKIRADSCGAIASERPVADYGVDI 235	DB 14;	SEQ ID NO: 32
Qy 236 VODIGRLVK --GSVEPYRVDLVSSFECAAGLGCGILSYABALLADESNTGNTYTKQYMLN 291	DB 15;	LENGTH: 1042;
Db 236 EQDTTRLDRERSAGTLQPTEL---KLMGASASLIKVYQTMFLQYQXQYQDHLS 291	DB 16;	TYPE: PRT
Qy 292 SYMDLSAAMRNALNMESKSDANKNPSLGLMNRCTAGMGKRLHMKLQPILDVEEN 351	DB 17;	ORGANISM: <i>Saccharomyces cerevisiae</i>
Db 292 QEMKLDSSAURALNLMGPGRDKSMSLFLNHNCKTPVGSRLIAQONKOPMLDAE 350	DB 18;	US-09-512-250C-32
Qy 352 CRDLVQSFVEDAALRQDLR-OHLKRISDTRLTHNLERKASLYHVWKLQYQSSTRVP-Y 409	DB 19;	Query Match Score 1571; DB 4; Length 1042;
Db 351 KROQLVEAFVNTNERQTMOCBEHLSRIPDYLXLRKFRQKQANLEDVYRYQVAILRPF 410	DB 20;	Best Local Similarity 38.4%; Pred. No. Be-139;
Qy 410 IKSVLERHDQFATLIRERYTIDSLEKWDSDDNHINKFIGIVETSYTSDQLENGEYMISSAY 469	DB 21;	Mismatches 324; Indels 96; Gaps 27;
Db 411 VNSLENVMDBEQYQTPLTEYTSNLSRSHSDS--LAKLEENVETTVYDALLENHETLIKPF 468	DB 22;	Qy 9 SKUPELKIDAKOAGGLFDRDDYTSHGDDATFLAFTYYHPTT 66
Qy 470 DPMLSAKLDQBTTLERQHINLHKQTANDLPLPIKSLKLKDQTFQGHVRITKKEEPKV 529	DB 23;	Db 79 STRBPLKFSDVSEERNFNFKYKTGLPKKKLKTRIVDKSDYTYTIGSDAFLVADSVYHPTQ 138
Db 469 DBSLRITRKCLDKGRHDGMGYEHRVARYDLDQDIEKZKLFLENHRYHGWCPRLTNESGCIR 528	DB 24;	Qy 67 ALR--QLG ---NRADLSSVSVSRNFETTIDVHEPKVTKVTSVLQVLATLKLCLID-LGKVKVEID-- -KGWLKLS 194
Qy 530 KQLNSHYIVLTERDQGVKFTYTKLKLGDQDQKIVKTYQKELVARYVQTAAASFSEV 589	DB 25;	Db 139 VLNKNCQLDQVTAKNFEHPTPKVTKVTSVLQVLATLKLCLID-LGKVKVEID-- -KGWLKLS 194
Db 529 NK--NEYQECCSTQRKGCVYFTTSTMQTLRRREHDQLSNTNTQGTGLVNEYVNVAASYCPVL 586	DB 26;	Qy 120 GTPGNLGSFEDILPANNEMQNSPVIAALAPNF-GQNG-CEVGLGYDITKRVIGLTETFD 177
Qy 590 AGIAGYTAELVLLSPADLARASCPTPYTRENISPDDTGILLEGRHPVCVAQDWNSIP 649	DB 27;	Db 195 ASPNTIEQYNELM--NMNIDSSTIATSKVQWNSQDGNCIGLIGVAFIDTAYKVGMIDTVD 252
Db 587 ERLAGYIAHLIVTIVSPAHASTHATFPYARXKMPHRPGTGTNTLKEARHPCMEMDDISFT 646	DB 28;	Qy 178 DSHTPNLSEALVALGCRELVPATGKSS--SEVRPMEDAISRGVMTTERKKTFRKGD 234
Qy 650 NDCLRYVGESEFOITGPNGCKSTYIROGVNVIMAQVSFVPCDNATSIRODIFARY 709	DB 29;	Db 253 NEVTSNLSFELIQVKGKECLVQDITNSNSNAEMQKVINIDRCGVTVLLRNSEBFSEKD 312
Db 647 NDVALYRDESSLFLITGPNGCKSTYIROGVNVIMAQTSFVPCTEAELIFDILARY 706	DB 30;	Qy 235 LVQDGLRGTGSVSPVRLQVSGF ---ECASGLGCILSYAELADEBNYNTVKQYN 289
Qy 710 GAGDCOLRGYSTEMQEMLETASILLAGTDSLIIDELGRSTSDFGFLWAICEHIVE 769	DB 31;	Db 313 VELDITLQGID----DIALSLSFQKYSKLSMGMCNALGYLQILSEQDQGVYELVHFK 366
Db 707 GASDSQLGTVSTFMAEMLETSNLKSATSELEIILIDELGRSTSDFGFLWAISEHIVT 766	DB 32;	Qy 290 LNSYNTMRDLSAAMPAINV-----MEKSDDANKNFSFLGMLNRTCTAGK 331
Qy 770 EIKAPPLFATFHETFLATANGNDNGHKNQGIANHVFPAHI----DESNRK---L 818	DB 33;	Db 367 LKEFMKLDA5A1KALNLFQGPQNPFFGGSNLLAVSGFTAGSNTGRTSDFQLLNF-CRTNA 425
Db 767 EIRCFGFLFATFHETLADAR---YPKS--VKNLHVVAFIGDGTDDSEDKSKRNQV 819	DB 34;	Qy 332 GKRLLHMMKQPLDQVBEINCRDLVQSVFVEDAALRQL-RQHLKRISDIERLTHNLERK 390
Qy 819 TMLYKHPGACDOSFGHVAFFANFPEPVVALAREQAESEDF----SPAI--- 866	DB 35;	Db 426 GVRLINEWLQPLTNIDELNKHLVQDIBLROMLTSEYLPMPIDIRRLTKKL-NK 484
Db 820 TILYRVEPGICDQSFGLVRAFPERKVNAMQAEELDFTSSEQDQSSMAIDKY 879	DB 36;	Qy 391 RASL1HVWLYQSOSTRVPTVKS1----ERHQGQFAYLIREXYDLSERKSDDNH-- 441
Qy 867 IPNDIKEAAS----KRKEFDRDHSRGTRATARQFLQDPLKMDPNTVYRQLS 919	DB 37;	Qy 485 RGNLDEVLKVIQFSKRIPEVQVQFTSFLEDDSPTEPVNELVRSWYLPL---SHVYEP 539
Db 880 SQQEEVERGSSQKELVQALVREIINITYTPEKLSVLAHDVLSFADDLASCPTPYTREN 620	DB 38;	Db 600 DPDKLKLKLEMHHLHGFWMRTRNDAKELRK--TRKYLSTVKAGIFSTKOKLSIANET 657
Qy 920 RM 921	DB 39;	Qy 561 QK1VEBEYKSQKELVQAAFSEFVAGIAVLAEDVLSFADDLASCPTPYTREN 620
		Db 658 NILQKEYDQKQSALVREIINITYTPEKLSVLAHDVLSFADDLASCPTPYTREN 717

Query Match 16.4%; Score 797; DB 4; Length 891;
 Best Local Similarity 27.8%; Pred. No. 8.3e-66;
 Matches 274; Conservative 177; Mismatches 375; Gaps 34;

4 NLEBQSKLPEKLDKQAQFSLPSFKTLPKDPRAVLFDR-RDYTTSHGDDATIAETTY 62
 5 NINKDIRYVVKIEMANITPMQOQYKIKSEYYDDCILFFFLGDFYEMFDKAEASRYLE 64
 63 HTTDTAURQLNTRADALSSVY---SRNPMTTARD---ILLERMRDTRLEYGSNW 114
 65 TLT-KRDAKKENP!PMCGPVPHYSADNTTLELINGYKVAICEOME---DPKQTKGMYR 119
 115 R-LVKSGTGPGLGSPFDILPAN-NEMONSPVIAALAAPNGCEVGLGYDITKRVLG 171
 120 REVVRITPGT-----VMONGMDEKNNYIL---SPTENE-EFGLYCDVSTGELK 167
 172 LTEFELDDSHFTNLLESVALVGCRECLVPAETGKSSERYPMFDAISRCGYMVTERRKKTEK 231
 168 VTHFKDTATLNN---EITTINPNEITV---KOALSPELKQROIINITE---TIVTREDISDE 219
 232 GRDLVDGLRIVKGSYVEPVRDLVSGPESAGALGICLSYBLLADESNYGNYTQYNLN 291
 220 DYDMNQLTHQIMHDTQULLYIHTHQKRD----LSHTE-----EVIEYAAV 262
 292 SYMRDSDAAMPAINTMNEKSKDANKNSFLSGLMNRTCTAGMGKRLLHMLKOPPLDVEEIN 351

Db 621 ISPPDT-GDILLEGGRHPCEVAQDWNSIPINDCLVLRGESWFQLIITGPNGGKSTYIarov 679
 Db 718 IHPMDSERTHLISRPYTFEMQDISFISIENDTLESGDFDILITGPNGGKSTYIrov 777
 Qy 680 GVNTLMAQGFSVCDNATISTRCTICAFYGAQDCQLCYSTFMQEMLETASTIKGATDR 739
 Db 778 GVISIMAQIGCFVPCEEAIAVAILCQVAGDSQLCGSTVFEILLETSILKRNASN 837
 Qy 740 SLLIDELPGTSPYDGFGLAWAICEHIVEIKAPTLPATHHELTALANKNDNGHKN 799
 Db 838 SLLIDELGRGTSPYDGFGLAWAIAEHLASKIGCFALFATHFELTELS-----EKL 889
 Qy 800 AGIANFHVAFAHDP-----NRKLTMLYKHGACDOSGFIHVAEFANFPSSVALAR 852
 Db 890 PVIQMHVYAHIEKONLKEQXHDDDTIYKVERQSISDOSRGHVAEVQPEKIVOKAK 949
 Qy 853 EKASeLDFSPAIATPNDIKEAASKRKRFDRDHVSRTGAROFLODFAQLPLDK--MD 91.0
 Db 950 RCANELDD---LKTNNEDLKK-----KLSQEVNEGNIKALLKEMIRKVKEEGLHD 1000
 Qy 911 PNUVQRQLSKMK 922
 Db 1001 PSKITEEASQHK 1012

RESULT 12
 US-09-134-001C-4913
 ; Sequence 4913, Application US/09134001C
 ; Patent No. 63,803,070
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: EPIDERMITUS FOR DIAGNOSTICS AND THERAPEUTICS
 ; TITLE OF INVENTION: STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064, 964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055, 779
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO: 4913
 ; LENGTH: 891
 ; TYPE: PRT
 ; ORGANISM: staphylococcus epidermidis
 ; US-09-134-001C-4913

Query Match 16.4%; Score 797; DB 4; Length 891;
 Best Local Similarity 27.8%; Pred. No. 8.3e-66;
 Matches 274; Conservative 177; Mismatches 375; Gaps 34;

4 NLEBQSKLPEKLDKQAQFSLPSFKTLPKDPRAVLFDR-RDYTTSHGDDATIAETTY 62
 5 NINKDIRYVVKIEMANITPMQOQYKIKSEYYDDCILFFFLGDFYEMFDKAEASRYLE 64
 63 HTTDTAURQLNTRADALSSVY---SRNPMTTARD---ILLERMRDTRLEYGSNW 114
 65 TLT-KRDAKKENP!PMCGPVPHYSADNTTLELINGYKVAICEOME---DPKQTKGMYR 119
 115 R-LVKSGTGPGLGSPFDILPAN-NEMONSPVIAALAAPNGCEVGLGYDITKRVLG 171
 120 REVVRITPGT-----VMONGMDEKNNYIL---SPTENE-EFGLYCDVSTGELK 167
 172 LTEFELDDSHFTNLLESVALVGCRECLVPAETGKSSERYPMFDAISRCGYMVTERRKKTEK 231
 168 VTHFKDTATLNN---EITTINPNEITV---KOALSPELKQROIINITE---TIVTREDISDE 219
 232 GRDLVDGLRIVKGSYVEPVRDLVSGPESAGALGICLSYBLLADESNYGNYTQYNLN 291
 220 DYDMNQLTHQIMHDTQULLYIHTHQKRD----LSHTE-----EVIEYAAV 262
 292 SYMRDSDAAMPAINTMNEKSKDANKNSFLSGLMNRTCTAGMGKRLLHMLKOPPLDVEEIN 351

Db 263 DYMMDYYAKRNILELTEESIRLKSKKGTLIWLMDETKTP-MGARRLKQWIDRPLLINKQQIN 321
 Qy 352 CRDLIVQSEVEDALRQDQHKRISIERLTHNLERKASLHVVKYOSSTRPVTK 411
 Db 322 DRNLNVEEMDRFETERDTRHNQVYTERLYGRVSYCNVNARDLQHKSSEIPHTK 381
 Qy 412 SVLERHDGGFATLIRRVTIDSLEKWSDDNHLNKEFIGLVETSV-----DLDQLENSE 462
 Db 382 ALNBNIGGTTTQKE-----LBP-----IDBLQIIFESLVEPPISIKDQGKFNG- 429
 Qy 463 YMISSAYDNLSALKD-----EQETLRQHNLHKQTANDLQLPDKSLKLDKETQRGH 516
 Db 430 -EFAQDQDXYLEASRKGKWHQWLABLQAKRERGTG-----KSLKISENKVRFGY 474
 Qy 517 VFRTKKCEPKVKQLNH-----YIYLETRKDGVKTYTQLKK-----LGQEQFKLYE 565
 Db 475 FIET-----RANLNNFOPEAFGYNKQTLNAERITDELKEKEIDLQGDAKVEL 527
 Qy 566 EYKSCQKELVARYVQTAASFSEVAGIGVLAEDVLSFADLAASCPTPYTPEPNISPD 625
 Db 528 EY-----ELFVKPKEHHTYTERLQKQKIISEDCLOSFAEZAK-YNYVKEPTES--D 578
 Qy 626 TGDIILEGGCRHPVCVE-ABDWNSTIPNDCLRLVGEBSWFOITQGMGGKSTYIRQGVNVL 684
 Db 579 DKVHLENSRHPVVERMDVNPNDCHL-DDEFITVLTGPMSGKSTYMQVAISI 637
 Qy 685 MAQGFSYPCDNATISIDCIFARVGADNCQLGQVSTFQMELTASLKGATDRSLII 744
 Db 638 MAQGAYYVCDSDATLPIPOQIFRIGAADDLVSCKSTPVMEBAQKALTYATENSLSLIF 697
 Qy 745 DELRGTSYDGFGRALWAIACEHIVEIKAPLTSFATHFELTALANKNGDNGHKNAGIAN 804
 Db 698 DEIERTGTSYDGFGRALQMIKXYAQTSFKTFLTHYHETSL-----DONLKCJCN 749
 Qy 805 FHYAHIDDSNRLKUMLYKVHPGACDQSFGIHVABFANPPSV----- 848
 Db 750 VHAA---NEYQGELIFLHKVQDGAVDDSYGIOVAKLADLPNEVTDRAQVILNAEQPKPSY 807
 Qy 849 ALAREKASEL-----DFSPLATIPNDTKEAASKRKFREFDRHDVSRGTARAROFLODFA 902
 Db 808 QLSHENTDQQTYSVSYNDFGRTEBEQSVECQIR----- 867
 Qy 903 QLPDKMDPNVNUVROKLSKMKTDLE 926
 Db 868 ELNUSNMNTLEALTKLNELQSLK 891

RESULT 13
 US-09-651-656-15
 ; Sequence 15, Application US/09651656
 ; Patent No. 634066
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCUTCHEON-MALONEY, SANDRA
 ; ADDRESS: LAWRENCE LIVERMORE NATIONAL LABORATORY
 ; TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
 ; POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
 ; TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
 ; FILE REFERENCE: IL-10689
 ; CURRENT APPLICATION NUMBER: US/09/651, 656
 ; CURRENT FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192, 764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SEQ ID NO: 15
 ; LENGTH: 819
 ; SOFTWARE: PatentIn Ver. 2.1
 ; TYPE: PRT
 ; ORGANISM: Thermus thermophilus
 US-09-651-656-15

Query Match 15.2%; Score 740.5; DB 4; Length 819;
 Best Local Similarity 29.2%; Pred. No. 1.6e-60;
 Matches 251; Conservative 136; Mismatches 312; Indels 161; Gaps 28;

35 PRAVLFDFRRYYTSHGDDATFIA-----ETYHHTTALRQGNRADALSSVSVSR 85
 Db 36 PDYLIFQDFYCFGEDERLARALGLVTHKTSKDTTPMAGIPIRA-----B5
 Qy 86 NMFFETIARDIL-----LEMFDRTLELYEGGSNWR-LVKSGTPGNLGSFEDILFANNEMQ 139
 Db 86 -FDAYAERUULKMGFRLAYADQVEAEEAEGLVREVTOLTTCTPL-TQEALL-----PR 137
 Qy 140 NSPVIAALAALPNFGONGCEVGLGYDITK----RVGLGLTEFDLDSHFTNLESALVALGR 194
 Db 138 EANVLAIAATGDN-----GLAFDVSTGEFKTLIKSKSALYDELFR-----
 Qy 195 ECLYPAETGKSSEYRPMFDAISRCGVMMTERKCKTEFKGRDLVQDGLRVTGSYEPVRDLV 254
 Db 183 ---PAEVLLAEPRE-----NEFAVAFKRKRPPVM---LSEAPPFQQGEGP 222
 Qy 255 SGFECAAGCAGCILSYAELJADESNYGNNTVKOYNL--NSYMRDLSAAMRALANMESKS 311
 Db 223 LALRRAQGA-----LAYAR----ATOQGALSVRPFLYDPEAFVRLPEASLKALEVFEPLR 275
 Qy 312 DANKNFSLGFLMUNPRCTAGMKRLLHMWKQPLLDVEEINORLQLVQSFYEDALRQDLR 371
 Db 276 QD-----TLEFGVLTDETRTA-FGRRLQJQAWLPHPLLERGLPLEARLDRVERFREGALREGTR 331
 Qy 372 QHLKRSIDIEBLTHNLERGRASLVHVKLYQSSTREVPTYKSVLERHDGFATLIRERYID 431
 Db 332 RLLFRIADLLEBLATRILESLRSAPRDLAALRSLLELPKGL-----
 Qy 432 SLEKNSDDNHLNKFLGVLTSVLDL-----ENGEYMISSAYDPNLNALXKD 478
 Db 374 -----LGEEVGLPDLGGLLEBLRAALIVEDPPLKVSSEGG--LIRESDPDLDALRR 421
 Qy 479 EOETLERQINHLHKQTANDLPLPDKSLKLKEQFHGPRTKKEPKYRKQLNNSHYIV 538
 Db 422 AHAEGVAYFLLEARKEERTGIP--TLKTYNAVEGYYLETRDYYEKVOE---YRP 474
 Qy 539 LETRDGVKFTYTKLGLDQFQKIVEYKSCQKELVARVQTAASFPEVAGLVAE 598
 Db 475 VOTLKDQRYTLPEKERELRYLQREALRERAKKEAELREARILAE 534
 Qy 599 LDVLLSFADLAAASCPTPYTRPNISPPTDGIDTLEGGCRHPCEVAODWVNISPNDCLVRGE 658
 Db 535 LDVYAAEAVR--HGYTRDRFGE---RURIRAGRHPYVERR-TAFVNDLEMAHE- 585
 Qy 659 SWFOILTGPNNNGKSTYIROYGVNVLMAQVSFVPCDNATATSIRODCIFARYGAGDCQLRG 718
 Db 586 -LVLTGPNAGKSTFLRQALIAIQSVPAAEELPLFDGJYTTGASDLAGG 643
 Qy 719 VSTPMQEMLETASILKGATDSLILIDELGGTSTDGFGLAWAICHEVIEKAPLTF 778
 Db 644 ESTFVYMEETAVLVLKEATERLVLDEVGRTSSLDGVATAALAE-ALHERRCYTLFA 702
 Qy 779 THFHEITALANKNGDNGHKNAGIANPHVFHIDPSNRKLMYKVHPGACDQSFRHVA 838
 Db 703 THYFELTALALPR-----LKNLHVVAKEEVEGG--LUVFYHQVLPGPASKSYGEVA 750
 Qy 839 EPANFPSSVVALEAREKSEL 858
 Db 751 ENAGLPKEVVERARALLSAM 770

RESULT 14
 US-09-650-055-15
 ; Sequence 15, Application US/09650855
 ; Patent No. 6363355
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCUTCHEON-MALONEY, SANDRA
 ; APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
 ; TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
 ; TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
 ; TITLE OF INVENTION: MISMATCHES
 ; FILE REFERENCE: IL-10284

; CURRENT APPLICATION NUMBER: US/09/650, 055
 ; FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192, 764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SEQ ID NO: 15
 ; TYPE: PRT
 ; ORGANISM: Thermus thermophilus
 ; US-09-650-055-15

Query Match 15.2%; Score 740.5; DB 4; Length 819;
 Best Local Similarity 29.2%; Pred. No. 1..6..60;
 Matches 251; Conservative 136; MisMatches 312; Indels 161; Gaps 28;

Qy 35 PRAVLFDFRDYTTSHGDDATFIA-----ETYHHTTALRQGNRADALSSVSVSR 85
 Db 36 PDYLIFQDFYCFGEDERLARALGLVTHKTSKDTTPMAGIPIRA-----
 Qy 86 NMFFETIARDIL-----LEMFDRTLELYEGGSNWR-LVKSGTPGNLGSFEDILFANNEMQ 139
 Db 86 -FDAYAERUULKMGFRLAYADQVEAEEAEGLVREVTOLTTCTPL-TQEALL-----
 Qy 140 NSPVIAALAALPNFGONGCEVGLGYDITK----RVGLGLTEFDLDSHFTNLESALVALGR 194
 Db 138 EANVLAIAATGDN-----GLAFDVSTGEFKTLIKSKSALYDELFR-----
 Qy 195 ECLYPAETGKSSEYRPMFDAISRCGVMMTERKCKTEFKGRDLVQDGLRVTGSYEPVRDLV 254
 Db 183 ---PAEVLLAEPRE-----NEFAVAFKRKRPPVM---LSEAPPFQQGEGP 222
 Qy 255 SGFECAAGCAGCILSYAELJADESNYGNNTVKOYNL--NSYMRDLSAAMRALANMESKS 311
 Db 223 LALRRAQGA-----LAYAR----ATOQGALSVRPFLYDPEAFVRLPEASLKALEVFEPLR 275
 Qy 312 DANKNFSLGFLMUNPRCTAGMKRLLHMWKQPLLDVEEINORLQLVQSFYEDALRQDLR 371
 Db 183 ---PAEVLLAEPRE-----NEFAVAFFRFPMV----LSEAPPFQQGEGP 222
 Qy 255 SGFECAAGCAGCILSYAELJADESNYGNNTVKOYNL--NSYMRDLSAAMRALANMESKS 311
 Db 138 EANVLAIAATGDN-----GLAFDVSTGEFKTLIKSKSALYDELFR-----
 Qy 195 ECLVPAETGKSSEYRPMFDAISRCGVMMTERKCKTEFKGRDLVQDGLRVTGSYEPVRDLV 254
 Db 183 ---PAEVLLAEPRE-----NEFAVAFFRFPMV----LSEAPPFQQGEGP 222
 Qy 255 SGFECAAGCAGCILSYAELJADESNYGNNTVKOYNL--NSYMRDLSAAMRALANMESKS 311
 Db 223 LALRRAQGA-----LAYAR----ATOQGALSVRPFLYDPEAFVRLPEASLKALEVFEPLR 275
 Qy 312 DANKNFSLGFLMUNPRCTAGMKRLLHMWKQPLLDVEEINORLQLVQSFYEDALRQDLR 371
 Db 276 QD-----TLEFGVLTDETRTA-FGRRLQJQAWLPHPLLERGLPLEARLDRVERFREGALREGTR 331
 Qy 372 QHLKRSIDIEBLTHNLERGRASLVHVKLYQSSTREVPTYKSVLERHDGFATLIRERYID 431
 Db 276 GQD-----TLEFGVLTDETRTA-FGRRLQJQAWLPHPLLERGLPLEARLDRVERFREGALREGTR 331
 Qy 372 QHLKRSIDIEBLTHNLERGRASLVHVKLYQSSTREVPTYKSVLERHDGFATLIRERYID 431
 Db 332 RLFLFRIADLLEBLATRILESLRSAPRDLAALRSLLELPKGL-----
 Qy 332 RLFLFRIADLLEBLATRILESLRSAPRDLAALRSLLELPKGL-----
 Db 374 -----LGEEVGLPDLGGLLEBLRAALIVEDPPLKVSSEGG--LIRESDPDLDALRR 421
 Qy 432 SLEKNSDDNHLNKFLGVLTSVLDL-----ENGEYMISSAYDPNLNALXKD 478
 Db 374 -----LGEEVGLPDLGGLLEBLRAALIVEDPPLKVSSEGG--LIRESDPDLDALRR 421
 Qy 479 EQETLEROTHNLHKSTANDLPLDPSKSLKDKEQFHGPRTKKEPKYRKQLNNSHYIV 538
 Db 422 AHAEGVAYFLLEARKEERTGIP--TLKTYNAVEGYYLETRDYYEKVOE---YRP 474
 Qy 539 LETRDGVKFTYTKLGLDQFQKIVEYKSCQKELVARVQTAASFPEVAGLVAE 598
 Db 475 VOTLKDQRYTLPEKERELRYLQREALRERAKKEAELREARILAE 534
 Qy 599 SWFOILTGPNNNGKSTYIROYGVNVLMAQVSFVPCDNATATSIRODCIFARYGAGDCQLRG 718
 Db 586 -LVLTGPNAGKSTFLRQALIAIQSVPAAEELPLFDGJYTTGASDLAGG 643
 Qy 719 VSTPMQEMLETASILKGATDSLILIDELGGTSTDGFGLAWAICHEVIEKAPLTF 778
 Db 644 ESTFVYMEETAVLVLKEATERLVLDEVGRTSSLDGVATAALAE-ALHERRCYTLFA 702
 Qy 779 THFHEITALANKNGDNGHKNAGIANPHVFHIDPSNRKLMYKVHPGACDQSFRHVA 838
 Db 703 THYFELTALALPR-----LKNLHVVAKEEVEGG--LUVFYHQVLPGPASKSYGEVA 750
 Qy 839 EPANFPSSVVALEAREKSEL 858
 Db 751 ENAGLPKEVVERARALLSAM 770

Qy 535 LDVYAAEAVR--HGYTRPRFGE--FLRIRAGRHPYVERR-TAFVNDLEMAHE- 585
 Qy 659 SWFOILTGPNNNGKSTYIROYGVNVLMAQVSFVPCDNATATSIRODCIFARYGAGDCQLRG 718
 Db 586 -LVLTGPNAGKSTFLRQALIAIQSVPAAEELPLFDGJYTTGASDLAGG 643
 Qy 719 VSTPMQEMLETASILKGATDSLILIDELGGTSTDGFGLAWAICHEVIEKAPLTF 778
 Db 644 ESTFVYMEETAVLVLKEATERLVLDEVGRTSSLDGVATAALAE-ALHERRCYTLFA 702
 Qy 779 THFHEITALANKNGDNGHKNAGIANPHVFHIDPSNRKLMYKVHPGACDQSFRHVA 838
 Db 703 THYFELTALALPR-----LKNLHVVAKEEVEGG--LUVFYHQVLPGPASKSYGEVA 750
 Qy 839 EFANFPSSVVALEAREKSEL 858

Db 751 EAGLPRKEVERARALISAM 770

RESULT 15
 US-09-651-656-1
 ; Sequence 1, Application US/09651656
 ; GENERAL INFORMATION:
 ; APPLICANT: MCCUTCHEON-MALONEY, SANDRA
 ; APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
 ; TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
 ; TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
 ; TITLE OF INVENTION: DNA DAMAGE AND DNA MISMATCHES
 ; FILE REFERENCE: IL-10389
 ; CURRENT APPLICATION NUMBER: US/09/651,656
 ; CURRENT FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192,764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 240
 ; TYPE: PCT
 ; ORGANISM: Homo sapiens
 ;
 US-09-651-656-1

Query Match 14.9%; Score 724.5; DB 4; Length 240;
 Best Local Similarity 62.4%; Pred. No. 6e-60; Gaps 3;
 Matches 153; Conservative 22; Mismatches 59; Indels 11;

Qy	635 RHPCVEAQDWNSIPIPNCDRLVRGESWFOILITGRNMGGKSTYTRQVGYNVLMHQVGSFVPC	694
Db	2 RHAACVEQDEIAFLPNDYFEKDQKMFLITGQVSTNQEMLETASILKGATDRSLIIIDELGRGTSTY	61
Qy	695 DNATISTRDCIFARVGAGSDCQRGVSTNQEMLETASILKGATDRSLIIIDELGRGTSTY	754
Db	62 ESAEAVSIUDCILARVGAGDSQLGVSTFMAEMLETASILSATAKDSLIIIDELGRGTSTY	121
Qy	755 DGRGLAWAICEHVEEIKAPTLFATHFEELTALANKDNGHKKNAGTANFVFAHDPS	814
Db	122 DGRGLAWAISEYATKIGAFCMFATHFEELTALAN-----QIPTVANNLFTAL--TT	171
Qy	815 NRKLITMLYKVHPGACDQSGFGIHVAEFANFPVVALAREKAABLEDSPIALPN-DIKE	873
Db	172 EETLTMLYQVKGVYCDQSGFGIHVAELANFPKVIECAKQAKALEEEFYIGGSQGVDIME	231
Qy	874 AASKR 878	
Db	232 PAAKK 236	

Search completed: April 7, 2004, 10:47:31
 Job time : 27 secs

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OM protein - protein search, using sw model

Run on: April 7, 2004, 10:46:01 ; Search time 53 Seconds
 (without alignment)
 4653.070 Million cell updates/sec

Title: US-10-029-065-2
 Perfect score: 4659

Sequence: 1 MNENLEQSKLPEKLDAKQAGPLSFKTLPKDPRARLFDRDYTSHGDDATFILET 60
 BLOSUM62 Scoring table: Gapext 10.0 , Gapext 0.5

Searched: 1071772 seqs, 262633353 residues

Total number of hits satisfying chosen parameters: 1071772

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:
 1: /cgns_6_ptodata/2/pubpaas/us07_pubcomb.pep:
 2: /cgns_6_ptodata/2/pubpaas/pct_new_pub.pep:
 3: /cgns_6_ptodata/2/pubpaas/us06_pubcomb.pep:
 4: /cgns_6_ptodata/2/pubpaas/us05_pubcomb.pep:
 5: /cgns_6_ptodata/2/pubpaas/us04_pubcomb.pep:
 6: /cgns_6_ptodata/2/pubpaas/us03_pubcomb.pep:
 7: /cgns_6_ptodata/2/pubpaas/us02_pubcomb.pep:
 8: /cgns_6_ptodata/2/pubpaas/us01_pubcomb.pep:
 9: /cgns_6_ptodata/2/pubpaas/us00_pubcomb.pep:
 10: /cgns_6_ptodata/2/pubpaas/us09b_pubcomb.pep:
 11: /cgns_6_ptodata/2/pubpaas/us09c_pubcomb.pep:
 12: /cgns_6_ptodata/2/pubpaas/us09_new_pub.pep:
 13: /cgns_6_ptodata/2/pubpaas/us10a_pubcomb.pep:
 14: /cgns_6_ptodata/2/pubpaas/us10b_pubcomb.pep:
 15: /cgns_6_ptodata/2/pubpaas/us10c_pubcomb.pep:
 16: /cgns_6_ptodata/2/pubpaas/us10_new_pub.pep:
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 18: /cgns_6_ptodata/2/pubpaas/us60_pubcomb.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
 US-10-029-065-2
 ; Sequence 2, Application US/10029065
 ; Publication No US20030150024A1
 ; GENERAL INFORMATION:
 ; APPLICANT: May, Gregory
 ; APPLICANT: Baszcynski, Christopher
 ; APPLICANT: Zhu, Tong
 ; APPLICANT: Kipp, Peter
 ; APPLICANT: Mahajan, Premod
 ; TITLE OF INVENTION: PLANT MSII SEQUENCES AND METHODS OF USE
 ; FILE REFERENCE: 5839-2 (035839/19619)
 ; CURRENT APPLICATION NUMBER: US/10/029, 065
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 939
 ; TYPE: PRT
 ; ORGANISM: Nicotiana tabacum
 ; US-10-029-065-2

Query Score Description
 Result No. Score Match Length DB ID
 1 4859 100.0 939 14 US-10-029-065-2 Sequence 2, Appli
 2 4856 99.9 939 14 US-10-029-065-4 Sequence 4, Appli
 3 3629 74.7 937 14 US-10-270-839-49 Sequence 49, Appli
 4 3082.5 63.4 860 12 US-10-425-14-56470 Sequence 56470, A
 5 2358 48.5 592 12 US-10-425-599-14104 Sequence 214104,
 6 2004.5 41.3 567 12 US-10-425-114-55750 Sequence 45750, A
 7 1842.5 37.9 934 14 US-10-109-791A-66 Sequence 66, Appli
 8 1841.5 37.9 934 9 US-09-788-57-19 Sequence 19, Appli
 9 1841.5 37.9 934 10 US-09-912-69-10 Sequence 10, Appli
 10 1841.5 37.9 934 10 US-09-760-28-20 Sequence 20, Appli
 11 1841.5 37.9 934 14 US-10-270-839-31 Sequence 31, Appli
 12 1841.5 37.9 934 14 US-10-243-130-11 Sequence 11, Appli
 13 1841.5 37.9 934 14 US-10-371-85-75 Sequence 5, Appli
 14 1841.5 37.9 934 14 US-10-371-634-9 Sequence 9, Appli
 15 1841.5 37.9 934 14 US-10-349-074-7 Sequence 7, Appli

Sequence 13, Appli
 Sequence 277, Appli
 Sequence 42582, A
 Sequence 3873, Ap
 Sequence 129, App
 Sequence 2022, App
 Sequence 37, App
 Sequence 65, App
 Sequence 125, App
 Sequence 172, App
 Sequence 174, App
 Sequence 284633
 Sequence 4999, Ad
 Sequence 11322, A
 Sequence 12632, A
 Sequence 1740, Ad
 Sequence 1983, A
 Sequence 1233, A
 Sequence 5274, Ad
 Sequence 44374, A
 Sequence 70970, A
 Sequence 11784, A
 Sequence 72450, A
 Sequence 51818, A
 Sequence 52510, A
 Sequence 53164, A
 Sequence 14767, A
 Sequence 2709, Ad
 Sequence 1315, A

Qy	181	FINLESALVALGCRCLVPAETGKSEYRPMFDAISRCGYWVTERKKTBFGKGRDILVDLG	240	US-10-029-065-4
Db	181	FTNLESALVALGCRCLVPAETGKSEYRPMFDAISRCGYWVTERKKTBFGKGRDILVDLG	240	
Qy	241	RIVKCSVEPYRDLVGFECASGALCILSYAELLADESNGNYTQKVNNSYMRDLSAA	300	
Db	241	RIVKCSVEPYRDLVGFECASGALCILSYAELLADESNGNYTQKVNNSYMRDLSAA	300	
Qy	301	MRALNMESRSANKNSFLFOLMNPCTAGKGRLLHMMWKOPLIDVEEINCRDLVQSF	360	
Db	301	MRALNMESRSANKNSFLFOLMNPCTAGKGRLLHMMWKOPLIDVEEINCRDLVQSF	360	
Qy	361	VEDAALRQDLRQLKRISDIERLTHNLERKASLYHVKLXQSSTRPVTIKSVLVERHDGQ	420	
Db	361	VEDAALRQDLRQLKRISDIERLTHNLERKASLYHVKLXQSSTRPVTIKSVLVERHDGQ	420	
Qy	421	FATLIBERYTIDSLEKSSDDNNLANKPTGLVETSVIDLQLENCEYMISSAYDPPNLSSALKDEQ	480	
Db	421	FATLIBERYTIDSLEKSSDDNNLANKPTGLVETSVIDLQLENCEYMISSAYDPPNLSSALKDEQ	480	
Qy	481	ETLEROQHNLHKOTANDLDLTDKLKDKEOTOFGHVFRITKEKEPKVQNLNSHYIVLE	540	
Db	481	ETLEROQHNLHKOTANDLDLTDKLKDKEOTOFGHVFRITKEKEPKVQNLNSHYIVLE	540	
Qy	541	TRKGVYFTYTKLKQKGDOFORTIVEYKSCORELARVVQTAASFSEPVAGLAGYLAEQ	600	
Db	541	TRKGVYFTYTKLKQKGDOFORTIVEYKSCORELARVVQTAASFSEPVAGLAGYLAEQ	600	
Qy	601	VILSFADLAASCPPTYTRPNTPPDGTDLILEGCRHPCEVAQDWNSIPNDNCRLYRGESW	660	
Db	601	VILSFADLAASCPPTYTRPNTPPDGTDLILEGCRHPCEVAQDWNSIPNDNCRLYRGESW	660	
Qy	661	POLITGPNMGKSTYTRQGVNLIAQGSFVPCDNATISRDCLFARYGQGDQLRGV	720	
Db	661	FQITGPNMGKSTYTRQGVNLIAQGSFVPCDNATISRDCLFARYGQGDQLRGV	720	
Qy	721	TNQEMLETASLKGATDRSLIIIDELGRGSTIDGFLGLWAIChIVEYKAPLFAH	780	
Db	721	TNQEMLETASLKGATDRSLIIIDELGRGSTIDGFLGLWAIChIVEYKAPLFAH	780	
Qy	781	FHELTALANKNDNGHKNAGIANFHVFIAHIDPSNRKLTMILYKVRGAACDSFGHVAEF	840	
Db	781	FHELTALANKNDNGHKNAGIANFHVFIAHIDPSNRKLTMILYKVRGAACDSFGHVAEF	840	
Qy	841	ANFPPSTVALAREKAASELDFSPITALPNDIKEAASKRKREFDRHDYSGRTARAOFLOD	900	
Db	841	ANFPPSTVALAREKAASELDFSPITALPNDIKEAASKRKREFDRHDYSGRTARAOFLOD	900	
Qy	901	FAQPLDKMDPNTVYRQLSKMKTDLERDAVDSHMLQOFF	939	
Db	901	FAQPLDKMDPNTVYRQLSKMKTDLERDAVDSHMLQOFF	939	
RESULT 2				
US-10-029-065-4				
; Sequence 4, Application US/10029065				
; Publication No. US2003/15002A1				
; GENERAL INFORMATION:				
; APPLICANT: May, Grzegoryski, Christopher				
; APPLICANT: Baszczyński, Christopher				
; APPLICANT: Zhu, Tong				
; APPLICANT: Kipp, Peter				
; APPLICANT: Mahajan, Pramod				
; TITLE OF INVENTION: PLANT MSH2 SEQUENCES AND METHODS OF USE				
; FILING DATE: 2001-12-20				
; CURRENT APPLICATION NUMBER: US/10/029, 065				
; SOFTWARE: Patent version 3.0				
; SEQ ID NO: 4				
; LENGTH: 939				
; TYPE: PRT				
; ORGANISM: Nicotiana tabacum				

RESULT 3
US-10-270-839-49

Sequence 49, Application US/10270839
; Publication No. US20030143586A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Luigi
; APPLICANT: Sabs, Philip M.
; APPLICANT: Nicolaides, Nicholas C.
; TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Diagnosis
; FILE REFERENCE: AG00023 (MOR_0133)
; CURRENT APPLICATION NUMBER: US10/270,839
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,750
; PRIOR FILING DATE: 2001-10-12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 49
; LENGTH: 937
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-270-839-49

Query Match 74.7%; Score 3629; DB 14; Length 937;
Best Local Similarity 72.4%; Pred. No. 2.7e-303; Matches 680; Conservative 137; Mismatches 118; Indels 4; Gaps 3;

Qy 1 MNENLEEQSKRLPELKDAQAOQGFLSFFKTLPKDPRAYRFLDRDYTTSHGDDATFIAT 60
Db 1 MEGNFEQNQNLPELKDAQAOQGFLSFFKTLNDTRAFDKDYYTAHGENSVFIATK 60

Qy 61 YHHTTALRQLGRADALSSVSVSRNMFTIARDILLERMDRTBLEYEGSGSNWRLYKSG 120
Db 61 YHHTTALRQLGSNALSSVISSRNMFTIARDILLERMDRTBLEYEGSGSNWRLYKIG 120

Qy 121 TPGNLSFEDILFANNEMONSPTAAALANFGONGCEYCYGLYTDITKRVLGIFELDDSH 180
Db 121 SPGNLSFEDILFANNEMODTPVVVSIFSDHGRCVIGMAYVDTLTERVYGLAEFLDDSR 180

Qy 181 FTNLESSIALGAKCIPPAESGSNECKSLYSLDSLERCAVMTTERKKHFKGRDLDSIK 240
Db 181 FTNLESSIALGAKCIPPAESGSNECKSLYSLDSLERCAVMTTERKKHFKGRDLDSIK 240

Qy 241 RLVKGSEPVYDLSGFECAGAGLCLTSYAEJLADAESENNGNTYKVOYNLNSTMRLDSA 300
Db 241 RLVGNIEPVYDLSGFEDILATPALGALLSFSELLSNEDNYNGNFTIRRVDIGFMRLDSA 300

Qy 301 MRALNVMESKSANKNSLFGLMNRTCTAGMGRPLHMLKQPLDVEINCPLDVSF 360
Db 301 MRALNVMESKSANKNSLFGLMNRTCTAGMGRPLHMLKQPLDVLNEIKTRLDIVCF 360

Qy 361 VEDAALRDLRQHLRISDELRTHNLERGRASLVHVVLYQSTRPVRVYKSVLRLHDQ 420
Db 361 VEAGLRDQIRQHLRISDELRTHNLERGRASLVHVVLYQSTRPVRVYKSVLRLHDQ 420

Qy 421 FATTLRERTIDSLEKMSDDNHLNKPIGLYETSYVLDOLENGEMISSAYDPNLSALDQE 480
Db 421 FASLISERVYKLCLEALSDQDHGKPIDLVCSVDDQLENGEMISSNDTKLASLXDK 480

Qy 481 ETLLERQHNLHKQTANDLIPIDESLKLKDKEFCHYFRTRKKEPKYVKQLNSHYIVL 540
Db 481 ELLBQOQHELHKKTAILEDQVDKALKLKDQAQFCHVFRTRKKEPKYVKQLTQFIVL 540

Qy 541 TRDGYKFTYTKLKLGDQPKTVEBKSYKSCQELYKSYKSCQELYKSYKSCQELYKSY 600
Db 541 TRDGYKFTYTKLKLGDQPKTVEBKSYKSCQELYKSYKSCQELYKSYKSCQELYKSY 600

Qy 601 VLLSPADLAASCPPTPYTRNTSPPTGDTILEGRHPVCYEQDWNSIPNDCRLVRGESW 660
Db 601 VLLSPADLAASCPPTPYCRPETSLDAGDVTEGSRHPVCYEQDWNSIPNDCRLMRGKSW 660

Qy 661 FQITGPNNMGKGSSTYTRQGVNVMAQVGSEVPCDNATISIRDCIFARYGAQDQLRGYS 720
Db 661 FQITGPNNMGKGSSTFTRQGVTVIMAQVGSEVPCDKASISIRDCIFARYGAQDQLRGYS 720

Qy 721 TENOQEMLTASTIRGATRSLLTIDELGRGTSTYDGFGLAWAICEHIVEEIKAPTLFATH 780
Db 721 TNOQEMLTASTIRGATRSLLTIDELGRGTSTYDGFGLAWAICEHIVEEIKAPTLFATH 780

Qy 781 FHETLALANKGD-NGHICKNAGTANFYFAHIDPSNRQLTMLYKVPGACDOSFGIHVAE 839
Db 781 FHETLALQANSESGN--TGVANFHSAHIDTESRQLTMLYKVPGACDOSFGIHVAE 838

Qy 840 FANPEPSTVALAREKAASLEDFSPAIPLNDIKEASSKREDFRDHVSRCGATARQFLQ 899
Db 839 FANPEPSTVALAREKAASLEDFSPSMINN-BESGKRSREDDPDEVSRGAERAHKLK 897

Qy 900 DFAQPLDIDPNVROULSKRMKIDLEDADAVDASHWLUOF 938
Db 898 ERAMPPLXMEKADSLSQRYREMDELEDAADCHWLRF 936

RESULT 4
US-10-425-114-56470
; Sequence 56470, Application US/10425114
; Publication No. US2004004888A1
; GENERAL INFORMATION;
; APPLICANT: Zhou, Jinhong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO: 56470
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB3219B02_FLI.pep
; US-10-425-114-56470

Query Match 63.4%; Score 3082.5%; DB 12; Length 860;
Best Local Similarity 68.4%; Pred. No. 3.1e-256; Mismatches 150; Indels 3; Gaps 3;
Matches 588; Conservative 119; Mismatches 150; Indels 3; Gaps 3;

Qy 82 SVSNMFETTARDILLEMDRTBLEYEGSGSNWRLYKSGSTGPNLGSFEDILFANNEMQNS 141
Db 2 SVSKAMFETIARNILLEDTCLTELEYEGSGSNWRLYKSGSTGPNLGSFEDILFANNMENS 61

Qy 142 PVITALAPNFGONGCEVGYGYVDTIKRVLGLTBFLDDSHFTNLESALVAGCERCLVPA 201
Db 62 PVITALAPFACRESOLVGLSFLDMTRKIGLAEPEDSRFTINVESALVAGCERCLVPA 121

Qy 202 TGKSEYREMFEDATSRCGYMVTKTFKGRDVLQDGLRVLVKGSGFECAS 261
Db 122 CERSIDLNLQDVTSNCNLLTEKKADEKSRLAQDGRIGRSVVRDLJSQFDAL 181

Qy 262 GALGCILSYAELLADESNYGNNTYKVOYNLNSTMRLDSA 321
Db 182 GPLGALLSYAELLADDTNNGNTYKTEKVNLYCNWRLDSA9VRLNIAEKTIDVKNFJFG 241

Qy 322 LMNRCTAGMGRLLHEMWLKPQPLDVEEINCRDLVQSVVEDAALRQLRQHJKRISDLE 381
Db 242 LMNRCTAGMGRLLHEMWLKPQPLDVEEINCRDLVQSVVEDAALRQLRQHJKRISDLE 301

Qy 382 RLTHNLERKASLHYHVKLYQSTRPVIKSYLVERHDGSOFTLJIREYIDSLEKWSDNH 441
Db 302 RLTHNLERKASLHYHVKLYQSTRPVIKSYLVERHDGSOFTLJIREYIDSLEKWSDNH 361

Qy 442 LNKRIGLVESTDQLENGEYMISSADPNSALKDQETLBRQINLHKQTANDLPLP 501
Db 362 FGRESSVLTETAILAQLENGEYRISPLSSDGLVYQSTRPVIKSYLVERHDGSOFTLJIREYIDSLEKWSDNH 421

QY 502 IDKSKLIDKETQGHYFRITKKEPKVKRQLNNSHIVYLETRKGKVFTYTKLKKLGQDFQ 561
 Db 422 VDKQKLKLEGS-QGHVFRNSKKEEQQVKRKLTGGLIIETRKGKVFTNKLKNLSDIQ 480
 QY 562 KIVBEYKSCQKELVARVTOATAFSEVAGIAGVIAEDVLISFDALAASCPPTPYTRPNI 621
 Db 481 ALFGEYTSQKVKYGVDTVRSGTSEVFENFAAVLSELVDYLOSPADLATSCPVPPYVRDI 540
 QY 622 SPPDGDILEGGCHRPVCBAQDWINSIPDCRLVRSHEWQQTGPNGGKSTYIRQVG 631
 Db 541 TRASPEDIVLGSRHPCLAEQDGINFIPNDCTLVRGKSFQQTGPNGGKSTYIRQVG 600
 QY 682 NVMQAQGSFVPCDNATISIRDCIFARVAGDCOLRGYSTEMQMLTASILKGATDSL 741
 Db 601 NVMLAQVGSSFPVPCDNATISIRDCIFARVAGDCOLRGYSTEMQMLTASILKGASDSL 660
 QY 742 IITDELGRGSTYDGFGLAWAICEHIVEETKAPTFATHFELTALANKNGD-NGHKKNA 800
 Db 661 IITDELGRGSTYDGFGLAWAICEHMEVTRAPTFATHFELTALAHNDDEHQHISDI 720
 QY 801 GIANHVFHAHDPSNRKLTMKYHPGACTDSFGTHVAFAANFPPSIVLAKEASELD 860
 Db 721 GVANYHVGAIHDPLSRKLTMKYVEPGACTDSFGTHVAFAANFTEAVVLAKSAAELED 780
 QY 861 FSPITATIPNDIK-EAASKRKEFRDRHDSRGATARQFLQDAOLPLKMDPNVVRQKL 919
 Db 781 FSTTPFSDLKDEVGSKXKRVFSSPDITRGAAARLFLFEAALPMDEMDSKILEMAT 840
 QY 920 KMKTDLERDAVDSHWLQQFF 939
 Db 841 RMKAQDQKDAADNPWLMQQFF 860

RESULT 5
 US-10-424-599-214104
 ; Sequence 214104, Application US/10424599
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovacic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53113)B
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO: 45750
 ; LENGTH: 567
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 701182994_FLI_pep
 ; US-10-424-599-214104

Query Match 48 5% Score 2358; DB 12; Length 592;
 Best Local Similarity 76.0%; Red. No. 4.9e-194;
 Matches 449; Conservative 68; Mismatches 72; Indels 2; Gaps 2;

QY 350 INCRDLYQSFEDALRQDQRHLKRISDLERLTNLERKASLYHVVKLYQSSTRVPY 409
 Db 1 INSRLLDVQAFEDTLRQDQRHLKRISDLERLTNLERKASLYHVVKLYQSSTRVPY 60
 QY 410 IKSVLERHDFGOFATLERYRLDSLEKWSDDHNLKPIGLVETSYDLDQLENGETMISSAY 469
 Db 61 IKSALERYDQGFSSTMRSRYLEPIELWTDDEHLNKIGLYVASVLDQLEMREIMSPY 120
 QY 470 DPNLSAALKDDETELLERQHNNHKCOTANDLDPIDSLKLUKJXETORGHVFTLKGKEPKV 529
 Db 121 DSILANLRQDQELLESQNLHRQTAADDLDPMDKALKLDRGTQFSGHVRFTLKGKEPKV 180

QY 530 KQLNSHYIVLTERKGKVFTYTKLKKLGQDFQKIVBEYKSCQKELVARVYQTAASFSYV 589
 Db 181 KUNTOQFILETRKGKVFTNKLKNLSDIQ 240
 QY 590 AGIAVGLIELDVLISFDALAASCPPTPYTRPNI SPPDGDILEGGCHRPVCBAQDWNSIP 649
 Db 241 ESELEITISBDVLISFDALAASCPPTPYTRPDTISSBEGDITLKGCHRCVCEAQDWNSIP 300
 QY 650 NDCLVRYGESWFMQFOLITGPMGGKSTYIRQGVNLYMAQGSFVPCDNATISIRDCIFARV 709
 Db 301 NDCLVRYGTMWFOLITGNGGKSTFIRQGVNLYMAQGSFVPCDNATISIRDCIFARV 360
 QY 710 GASDQCOLGCVSTMQMLTASTLKGATDSLIIIDELGRGSTYDGGLAWAICEHVE 769
 Db 361 GASDQCOLGCVSTMQMLTASTLKGATDSLIIIDELGRGSTYDGGLAWAICEHVE 420
 QY 770 EIKAPTLBATHFELTALANKNDNGHKN-AGIANFIVPAHDPNSKLTMKYVHFGA 828
 Db 421 VIKAPTLBATHFELTALALEVNSDSDQKQIVGANTVSAHIDSSTEKLTMKYVKEFGA 480
 QY 829 CDOSFGHIVAEAFANFPPSVYALAREKASELDSPSIAL-IPIIDKEAASKRKEFRDHDV 887
 Db 481 CDQFGHIVAEAFANFPEVSUTLAREKAELEDSPSATSLSNHTTQEVSQSKRAFEPPDM 540
 QY 888 SRGTARARQFLQDAQLPKMDPNVUVQQLSKMKTDLERDAVDSHWLQQF 938
 Db 541 SOGAKAKRQFLFEEAVLPIPETMKMQLAEVQKLTDIJEKDARNCNWQF 591

RESULT 6
 US-10-425-114-45750
 ; Sequence 45750, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53113)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO: 45750
 ; LENGTH: 567
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 701182994_FLI_pep
 ; US-10-425-114-45750

Query Match 41.3% Score 2004.5; DB 12; Length 567;
 Best Local Similarity 67.3%; Pred. No. 1.4e-163;
 Matches 388; Conservative 80; Mismatches 103; Indels 3; Gaps 3;

QY 374 LKRISDLERLTNLERKASLYHVVKLYQSSTRVPYIKSVLERHDQFATLERYRLDSL 433
 Db 1 LKRISDLERLTNLERKASLYHVVKLYQSSTRVPYIKSVLERHDQFATLERYRLDSL 60
 QY 434 EKWDSDNNHLNKFLIGLVETSYDLDQLENGETMISSAYDNLSAKDEQETLEROIHNHQ 493
 Db 61 EWMKAKNRGFRSSVETAILQLENGETYRISPLYSSDGLVKELSVVENHTINNUHYD 120
 QY 494 TANDLDPIDSLKLUKJXETORGHVFTLKGKEPKVQKDNHRYTLETRKGKFTYKL 553
 Db 121 TASDDLSVDQKLXKLGKGS-LGHYFRMSKKEQKVRKLTGSYLLIEERKGKFTNSKL 179
 QY 554 KKLGDPQKIVBEYKSCQKELVARVYQTAASFSYVAGTAGVIAELDYLVLSFADLASCP 613
 Db 180 KNLSDQYQALFGETYSCKKVGDVVRSGTFSFVFNFAAVLSDVLDQSFADLATSSCP 239

Qy 614 TPTYTRNISPPDGTIDILEGCRHPCVEAQDWINSIPNDCLRLVRGESWFOITGPNNCGKS 673
 Db 240 VPIVPRD:TASIDGDIVLGSRPECLEQDGTFNIFINCTLRGSKFQITGPNNCGKS 299
 Qy 674 TYTROGVYNLMAQVGSTPVCNDATISTRDCFCARYGAGDCQLRGYSTMQEMLETASIL 733
 Db 300 TPTROGVYNLMAQVGSPVCDOSISVRDCTFCARYGAGDCQLRGYSTMQEMLETASIL 359
 Qy 734 KGATDRSLIIIDLGRTSYTDGLAMAICHIVEEIKAPLFAITHFELZALANKGD 793
 Db 360 KGASDKSLIIIDLGRTSYTDGLAWAICHILMEVTRAPTFELTHAHNND 419
 Qy 794 -NGBHKNGANLPHVFAIDPSNRKLTMLYKVPGACDSFGHVAEFANFPSPVALAR 852
 Db 420 EHGHTSDIGVANTHVGHHIDPLSRKLTMLYKEPGACDSFGHVAEFANFPSPVALAR 479
 Qy 853 EKASELDTSPIALIPINDK-TAAASKRKREFRDHRDVSRTATAROFLQDFALPLDKMDP 911
 Db 480 SKRAELEDTSPTFSDDLKDEVGSKRGRVFSDDITRGAAARLFLFEEALPMDENG 539
 Qy 912 NTVRKQLSKMKTLERDAVDSHWLQQFF 939
 Db 540 SKLEMATKOMADLQKDAADNPWLMQFFF 567

RESULT 7
 US-10-109-791A-66
 ; Sequence 66, Application US/10/09791A
 ; Publication No. US20030138787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BiTech Oncologic Corp.
 ; TITLE OF INVENTION: Functional Genetic Tests of DNA Mismatch Repair
 ; FILE REFERENCE: BTOL 102 NP
 ; CURRENT APPLICATION NUMBER: US/10/109, 791A
 ; CURRENT FILING DATE: 2002-09-06
 ; NUMBER OF SEQ ID NOS: 315
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 66
 ; LENGTH: 934
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-109-791A-66

Query Match Score 37.9%; Score 1842.5; DB 14; Length 934;
 Best Local Similarity 43.0%; Pred. No. 2.9e-149; Gaps 19;
 Matches 403; Conservative 172; Mismatches 307; Indels 55;

Qy 14 LKUDAKOQGELSFKKTLPKDP-RAVRLFDRDYTTSHGDDDTIAFTTYHTTTALRQLG 72
 Db 9 LOQESAAEVGFREFQGNBKEPKTTVRLFDRDYTTSHGDDDTIAFTTYHTTTALRQLG 68

Qy 73 NR-ADALSSVSYSRNMFTTARDILLERMRTDLYEGSGSN----WRLVKSGTPGN 124
 Db 69 PAGAKNQSVVLSKMNFFSVDKDLLYTQYR-VEVYKRNAGRKAASKENDWYAYKASPQN 127

Qy 125 LGSPFEDLFANENMQNSPVIAALAPNPFQONGVLPDFTVRLFDRDYTTSHGDDDTIAFTTYHTTTALRQLG 184
 Db 128 LSQFEDLFGNNDMSMASIGVVKUMSAVDQGVGTVDSIORKLGICEFFNDQFSNL 187

Qy 185 ESALVALGCRCVLP-AET-GKSSSEYRPMDAISRCGYMVTREKKTEFKGRDLVODIGRL 242
 Db 188 EALLIQIGPCKCVLP-GGETAGDNGKLRLQ---TQRGGGLLITERKKADEFSTKDLYQDANR 244

Qy 243 VKG-----SVEPVRDVLVSGFECASGALGCLSYAELADESNYGNTVQYQNLNSYM 294
 Db 245 LKCKKGKGEQNSAVLPEME---NOVAYVSSLAVTKFJELLSDSNFQGCFELTTFDSFQYM 300

Qy 295 RLDQAAMRALNWN-SKSDANRNFSLFGJGMNRTCTAGNGKRLHMKWIKOPLDVBEEINCR 353
 Db 301 KLDIAAVRALNLFQGSVDETDQSLLAIIINK-CKTPOGQRLYNQWIKOPLDKNRLEER 359

Qy 354 LDVYQSQSFEDALRQD-LRQH-LKRIISDIERLTHNLERGRASLYHVVLYQOSTSTRVPIKS 412

Db 360 INLVAFTEVEDAELROTQEDLJRRREPDLNRLAKKFQDQANIQDCVRYLQGINOLPNVHQ 419
 Qy 411 VLERHDGGFATLTERVIDSLEKWDNHNKPIGLVETSVIDLQLENCEYMISSADPN 472
 Db 420 ALEXHECKHQKLAVVTP-TDLRSD- -FSKEQEMETLDMQVETTFLVKPSPFPN 477
 Qy 473 ISALKDCEFTLERQHNLHKOTANDLPLIDKSLKLDRKETOFGHVFRITKKEPKVQYQL 532
 Db 478 LSELREIMNDLERQKMQSLISIARDLGJDPGQIKLSSAQGQYYFRTICKERKVLN-- 535
 Qy 533 NSHYIVLETRKDQGVKETYTKLKKLGDOFQKIVYEYKSQKELYARRYQTAASFSEVFAGI 592
 Db 536 NKFNSTVDIQRNGVKFTNSKCTSLNEEFYTKNTRKEYBEAADATVKEITNISGYVEPMQTL 595
 Qy 593 ACTYLAEELDVLISPADLASSCPYPYTRPNISPDTGDLILEGRHPYCVAQDWINSIPTDC 652
 Db 596 NDYLAQDIAVSYFAHVSNGAPVPPVREALEKGQGRILKASRHACYVQDETAFIPINDV 655
 Qy 653 RLVRGEWSFQITGPNNCGKSTYIROYGVNTIMAQVGSFVPCDNATISIRDCIFARYGAG 712
 Db 656 YFEKDQMFHITGPNNCGKSTYIROYGVNTIMAQVGSFVPCSAEYSVDCILARYGAG 715
 Qy 713 DCOLRGYSTFMQEMLSTSILKGATDRSLIITDELGRGTSYDGFGLWAICBHVIEPIK 772
 Db 716 DSOLKGYSTFMQEMLSTSILKGATDRSLIITDELGRGTSYDGFGLWAICBHVIEPIK 775

RESULT 8
 US-09-788-657-19
 ; Sequence 19, Application US/09788657
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaides, Nicholas
 ; APPLICANT: Sass, Philip
 ; APPLICANT: Kinzler, Kenneth
 ; APPLICANT: Grasso, Inigo
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Methods for generating hypermutable
 ; TITLE OF INVENTION: Yeast
 ; FILE REFERENCE: 011-07-00097
 ; CURRENT APPLICATION NUMBER: US/09/788, 657
 ; CURRENT FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: 60/184, 336
 ; PRIOR FILING DATE: 2000-02-23
 ; NUMBER OF SEQ ID NOS: 25
 ; SEQ ID NO: 19
 ; LENGTH: 934
 ; SOFTWARE: Fast-SEQ for Windows Version 3.0
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-788-657-19

Query Match Score 37.9%; Score 1841.5%; DB 9; Length 934;
 Best Local Similarity 43.0%; Pred. No. 3.6e-149; Gaps 19;
 Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

Qy 14 LKLDAKQAGELSFKKTLPKDP-RAYTFLFDRDYTTSHGDDDTIAFTTYHTTTALRQLG 72
 Db 9 LOQESAAEVGFREFQGNBKEPKTTVRLFDRDYTTSHGDDDTIAFTTYHTTTALRQLG 68

Qy 73 NR-ADALSSVSYSRNMFTTARDILLERMRTDLYEGSGSN----WRLVKSGTPGN 124
 Db 69 PAGAKNQSVVLSKMNFFSVDKDLLYTQYR-VEVYKRNAGRKAASKENDWYAYKASPQN 127

Qy 125 LGSPFEDLFANENMQNSPVIAALAPNPFQONGVLPDFTVRLFDRDYTTSHGDDDTIAFTTYHTTTALRQLG 184
 Db 128 LSQFEDLFGNNDMSMASIGVVKUMSAVDQGVGTVDSIORKLGICEFFNDQFSNL 187

Qy 185 ESALVALGCRCVLP-AET-GKSSSEYRPMDAISRCGYMVTREKKTEFKGRDLVODIGRL 242
 Db 188 EALLIQIGPCKCVLP-GGETAGDNGKLRLQ---TQRGGGLLITERKKADEFSTKDLYQDANR 244

Qy 243 VKG-----SVEPVRDVLVSGFECASGALGCLSYAELADESNYGNTVQYQNLNSYM 294
 Db 245 LKCKKGKGEQNSAVLPEME---NOVAYVSSLAVTKFJELLSDSNFQGCFELTTFDSFQYM 300

Qy 295 RLDQAAMRALNWN-SKSDANRNFSLFGJGMNRTCTAGNGKRLHMKWIKOPLDVBEEINCR 353
 Db 301 KLDIAAVRALNLFQGSVDETDQSLLAIIINK-CKTPOGQRLYNQWIKOPLDKNRLEER 359

Qy 354 LDVYQSQSFEDALRQD-LRQH-LKRIISDIERLTHNLERGRASLYHVVLYQOSTSTRVPIKS 412

CURRENT APPLICATION NUMBER: US/09/912,697
 CURRENT FILING DATE: 2001-07-25
 NUMBER OF SEQ ID NOS: 39
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 10
 LENGTH: 934
 TYPE: PCT
 ORGANISM: Homo sapiens
 US-09-912-697-10

Query Match Score 37.9%; Best Local Similarity 43.0%; Pred. No. 3.6e-49; Mismatches 307; Indels 55; Gaps 19; Matches 403; Conservative 172; NR-ADALSSVSYRNMPETIARDILLERMDRTLEGGSGSN-----WRIVKSGTPGN 1.24

Db 69 DAKARNLSSVUSKRNKFESTFVKDILLTRQYR VEVYKRNRAKSKENDWIAKYKSPGN 1.27

Qy 125 LGSFEDILFANNEQNPSVIAALAPNFQNGCCEVGLGVDTKRVLGILTTEFLDDSHFTNL 1.84

Db 128 LSQFEDIFGNNDNSASATGIVGMSAVDQGRYGVGVPDS QRKGCLICEFFDNDQESNL 1.87

Qy 185 ESNALVAGCPECLP-AET-GKSSEXYRPMDAISRCGYMMTEBKKEFKGRDLYVIDGLR 2.42

Db 188 EALIIOQGPKECVLPGGETAGDNGKLRLQI---IQRGGLILTRKGADFSTKTYQDINRL 2.44

Qy 243 VRG -----SVEPVDRLVGPFECASGALGCTLSYABLADESNGNYTQYQNLNSYM 2.94

Db 245 LKGKKGEMQNSAVLPENE---NOVANVSSAVKFLLEUDSNSFGOFELUTDFEQM 3.00

Qy 295 RLDESAAMRALNVM--SKSDANKNSFLGELMNRTAGMKRLLHMWKQPLLDVEEINCR 3.53

Db 301 KLDAAVRLNLNFGQSVEDTTGSOSLALLNK-CKTPQGRLYQWTKPQMLDKNR-BER 3.59

Qy 354 LDIVOSFEDAALRDQDZQH-LKBDISDLERLTHNLERKASHVHVVKLYQOSSTRPVYIKS 4.12

Db 360 ONLYBAFEDAEIRQTOLQDLRERFDINRLRACKFQRQANLQDCYRXYQGQNOLPNVTQ 4.19

Qy 413 VLERHDQGPATLERYIDSLEYMSDDNHLNKFGLVETSVDQDLENGEYMISSAYDPN 4.72

Db 420 ALEFCHEGHQKLLAVFLAVFPTPLTDLRSR-D-FSKQEMIETLMDQDVENHEFLYKPSFPDN 4.77

Qy 473 LSALKDQETTLERQHNLHKOTANDLDPIDSKLMLKDETOFGHVERTRTKREPKVRKQL 5.32

Db 478 LSELREIMNDLEKGMQSTLISAAARDLQDPGQKIKLSSAQFYFRTCKEKEVLRN-- 5.35

Qy 533 NSHYTVLTERKDGKFETYKLUKKGDOFOKITVEEYKSCOKELYARVVOTAAFSFVEFGI 5.92

Db 536 NKNFSTVDIQKNGKFTNSKLTSLNEEYTKNTKTEVEEAQDAIVEKVNNSGTVEPMTL 5.95

Qy 593 AGVLAEDLVLSFADLAASCPPTPYTRNPNSPPDGTDLLEGCRHPVCVAQDWYNSIPND 6.52

Db 596 NDVIAOLDATAVSFAITVNSGAPVPTVRAFILEKGQRTTILKASRACEVQEDEAFIPNDV 6.55

Qy 653 RLVRGESWFOQITGPNGMGKSTYIQRGVGUNVLMQGVSPYPCDNATISIRDCTIPARVGAG 7.12

Db 656 YFEKDQMFHITGPNGMGKSTYIQRGTGVUMLMQIGCFVPCESAEVSTYDCILARVGRG 7.15

Qy 713 DCOLRGYSTMOEMLETASTIKGATDRLIITIDELGRGTSTYDGFGLAWAICEHIVEEK 7.72

Db 716 DSQJQGVSTFNAEMLETASLIRSAYKDSLITIDEIQRGTSTYDGFGLAWAISEYIATKIG 7.75

Qy 773 APTLFATHETHETLATANKDNGHKKNAGTAANFHVFYAHIDPSNRNLKTMLYKVHGPACDOS 8.32

Db 776 AFCMATPHETHTALAN-----QIPTYNLHYLT-TTEETLTMLYQVKRKEVCDOS 825

Qy 833 FGIIHYAEFANPPSVVALAREKASELEDPSIAIIPN-DIKEAASKR--KREFDRHDVS 8.88

Db 826 FGIIHYAELANFPKHIECAKQKALEEFTQYIGESEGYDIMEPAKXCYLRE----- 8.78

Qy 889 RGTARARQFLDFAQULPLKNDPNTVYRQKLSRMKCDL 9.05

Db 879 QGEKIIQEFLSKVKQMFETENSEENITIKLQKLKAEV 9.15

RESULT 9
 US-09-912-697-10
 Sequence 10, Application US/09912697
 Publication No. US20030068800A1
 GENERAL INFORMATION:
 APPLICANT: Nicolaides, Nicholas C
 APPLICANT: Sassi, Philip M
 APPLICANT: Grasso, Luigi M
 APPLICANT: Kline, J Bradford
 TITLE OF INVENTION: METHODS FOR GENERATING ANTIBIOTIC RESISTANT MICROBES AND NOVEL
 FILE REFERENCE: MOR-0040

Qy 833 FGIIHYAEFANPPSVVALAREKASELEDPSIAIIPN-DIKEAASKR--KREFDRHDVS 8.88
 Db 826 FGIIHYAELANFPKHIECAKQKALEEFTQYIGESEGYDIMEPAKXCYLRE----- 8.78

QY 889 RGTTARAOFLQDFALQPLDMDPENVRQKLSKMKTDL 925
 :
 Db 879 QGEKLIQEFLSKVQMPFTEMSEENITIKLQLKAEV 915

RESULT 10
 US-09-760-285-20
 ; Sequence 20, Application US/09760285
 ; Publication No. US20030091997A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Grasso, Luigi M.
 ; APPLICANT: Sassi, Phillip M.
 ; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
 ; FILE REFERENCE: MOR-0017
 ; CURRENT APPLICATION NUMBER: US/09/760,285
 ; CURRENT FILING DATE: 2001-01-15
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 20
 ; LENGTH: 934;
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-760-285-20

Query Match 37.9%; Score 1841.5; DB 10; Length 934;
 Best Local Similarity 43.0%; Pred. No. 3.6e-149;
 Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 IKLDAKOAGQELSFPEKTKLPDP-PAVRLFDRDYTTSHHDDATTAETYYHTTAIRQG 72
 9 LQLEAAEVCFVRPQGMPPRPTTVRLFRGDFTAHGDEALLAAREYFKTQCVIKNG 68

QY 73 NR-ADALSSVSYSRNMPETTARDILLERMDRTILEYEGSCSN-----WRLVKGSGTPN 124
 69 PAGAKNLQSTVSLSKNPFESTVKDQJLIVROYR-VEYVKNRAGKASKENDWLAYKASPN 127

QY 125 LGSPFDILFANEMMONSPVIALAPNFGONGCEVGLGYDITKEVGLATEFLDDSHFTNL 184
 128 LSQOFDILEFGNDMSASIGVGVKMSAVDGQRQVGVTYDSDIQKLGLCEFPDNDQFSNL 187

QY 185 ESALVALGCRECLYP-AET-GKSSEYRPMFDAISRCGVNYTERCKTEFKGRDLYQDGLR 242
 188 EALLIQIGPKCBLPGGETTAGDMGKLQR1--IORGGLITERKAADFSTDYQDNLRL 244

QY 243 VKG-----SVEPYRDLVGFFECASGAIGCILSYAELADESNYGNTYKQYNLNSYM 294
 245 LKGKGEQMNNSAVLFEME---NOVAVASSAVKPLELSDDNFGQFELTTEDFSQM 300

QY 295 RLDSSMRMLNVM-EKSDANKNFSLFLGMNRTCTAGMGKRLIMWLKOPLDVEEINGR 353
 301 KLDAAVRAVLNLFQGSVDTGSQLAALINK-CTKPOGRLYNNQWIKPLMKRNER 359

QY 354 LDLYQSFSVEDAALRDLRQH-LKRISDIBRTHNLERKASLVHIVVKQYQSTRPVYIKS 412
 360 LNLFVERAIVEDLRLROTQDLLRRPDPNLNLAKEFQRQAQNLDQCYRLIQGNGOLPNVHQ 419

QY 413 VLERHDQGPATLIREYITDSLEKSSDDNHLNKFLIGLVERSVDLDOLENGEYMISSAYDPN 472
 420 ALEXKEGHQKLLAVFVPTPLTDLSRD--FSKQFEDMIDMVOHENEFLYKPSFEDN 477

QY 473 ISALKDEQETTLERQHNLHKQTANDLDPDKS1KLKDKEFQHGFVTRKCEEPKVKRQL 532
 478 LSELREBIMNDLEKMQNSTLISAAARDLGDPGKQKLDSAAQFGYFYRTCKEKEVLRN-- 535

QY 533 NISHYTVLETRDGVKFETYTKLKLQDFQKVEEYKSCOREVYQTAASFSEVFAGI 592
 536 MKNFSTVDIOKNGKFTNSKTSLSNEEYTKNTKTEYEAAQDIAVEKVNNTSSGYVEPMOTL 595

QY 593 AGVIAELDVLISFLADLAASCPTPYTRNPISPDTGDIILEFGCRHPCEAQDWINSIPND 652
 596 NDVLAQDVAWSFAVPSANGAQPVTPRPALEKGQPRITKURSAACVEQDIAFIPNDV 655

Db 713 DCOLRGVSTPMQEMLETASTLKGATDRSLTIDELGRGTSTYDGFGLAWAICEHVEIK 772
 Db 716 DSQLRGVSTPMQEMLETASLRSATKDSLTIIDEGRGTSTYDGFGLAWAISETATV 775

QY 773 APLTFATHPEHETLANKNGDNGKKKAGIANFHVPAHIDPSNRKLTMLYKUHPGACDQS 832
 Db 776 AFCMFATHPEHETLANT-----QIPTVNNLHVITAL-TTEETLTMXQVKRGCVCDQS 825

QY 833 FGIVYAFANFPPSVVALLAREKASLEDSPESIALIPN-DIKEAASKR--KREFDRHDVS 888
 Db 826 FGIVYAEELANFPKHVIECAKQKALEBFQYIGESQGDIMEPAKKCYLERE----- 878

QY 889 RGATARARQFLQDPAOLPDKMDPNVVRQKLSKMKTDL 925
 Db 879 QGEKLIQEFLSKVKOMPTEEMSEENITIKLQLKAEV 915

RESULT 11
 US-10-270-839-31
 ; Sequence 31, Application US/10270839
 ; Publication No. US20030143586A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chao, Qimin
 ; APPLICANT: Grasso, Luigi
 ; APPLICANT: Sassi, Phillip M.
 ; APPLICANT: Nicolaides, Nicholas C.
 ; TITLE OF INVENTION: Genetic Hypermutability of Plants for Gene Discovery and Di-
 ; CURRENT APPLICATION NUMBER: AG0002US (M0R-0133)
 ; CURRENT FILING DATE: 2002-10-27
 ; PRIORITY APPLICATION NUMBER: 60-328,750
 ; NUMBER OF SEQ ID NOS: 129
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 31
 ; LENGTH: 934
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-270-839-31

Query Match 37.9%; Score 1841.5; DB 14; Length 934;
 Best local Similarity 43.0%; Pred. No. 3.6e-149;
 Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

QY 14 IKLDAKOAGQELSFPEKTKLPDP-RAVRLFDRDYTTSHHDDATTAETYYHTTAIRQG 72
 9 LOLEAAEVCFVRPQGMPPRPTTVRLFRGDFTAHGDEALLAAREYFKTQCVIKNG 68

QY 73 NR-ADALSSVSYSRNMPETTARDILLERMDRTILEYEGSCSN-----WRLVKGSGTPN 124
 69 PAGAKNLQSTVSLSKNPFESTVKDQJLIVROYR-VEYVKNRAGKASKENDWLAYKASPN 127

QY 125 LGSPFDILFANEMMONSPVIALAPNFGONGCEVGLGYDITKEVGLATEFLDDSHFTNL 184
 128 LSQOFDILEFGNDMSASIGVGVKMSAVDGQRQVGVTYDSDIQKLGLCEFPDNDQFSNL 187

QY 185 ESALVALGCRECLYP-AET-GKSSEYRPMFDAISRCGVNYTERCKTEFKGRDLYQDGLR 242
 188 EALLIQIGPKCBLPGGETTAGDMGKLQR1--IORGGLITERKAADFSTDYQDNLRL 244

QY 243 VKG-----SVEPYRDLVGFFECASGAIGCILSYAELADESNYGNTYKQYNLNSYM 294
 245 LKGKGEQMNNSAVLFEME---NOVAVASSAVKPLELSDDNFGQFELTTEDFSQM 300

QY 295 RLDSSMRMLNVM-EKSDANKNFSLFLGMNRTCTAGMGKRLIMWLKOPLDVEEINGR 353
 301 KLDAAVRAVLNLFQGSVDTGSQLAALINK-CTKPOGRLYNNQWIKPLMKRNER 359

QY 354 LDLYQSFSVEDAALRDLRQH-LKRISDIBRTHNLERKASLVHIVVKQYQSTRPVYIKS 412
 360 LNLFVERAIVEDLRLROTQDLLRRPDPNLNLAKEFQRQAQNLDQCYRLIQGNGOLPNVHQ 419

QY 413 VLERHDQGPATLIREYITDSLEKSSDDNHLNKFLIGLVERSVDLDOLENGEYMISSAYDPN 472
 420 ALEXKEGHQKLLAVFVPTPLTDLSRD--FSKQFEDMIDMVOHENEFLYKPSFEDN 477

QY 473 ISALKDEQETTLERQHNLHKQTANDLDPDKS1KLKDKEFQHGFVTRKCEEPKVKRQL 532
 478 LSELREBIMNDLEKMQNSTLISAAARDLGDPGKQKLDSAAQFGYFYRTCKEKEVLRN-- 535

QY 533 NISHYTVLETRDGVKFETYTKLKLQDFQKVEEYKSCOREVYQTAASFSEVFAGI 592
 536 MKNFSTVDIOKNGKFTNSKTSLSNEEYTKNTKTEYEAAQDIAVEKVNNTSSGYVEPMOTL 595

QY 593 AGVIAELDVLISFLADLAASCPTPYTRNPISPDTGDIILEFGCRHPCEAQDWINSIPND 652
 596 NDVLAQDVAWSFAVPSANGAQPVTPRPALEKGQPRITKURSAACVEQDIAFIPNDV 655

Db 713 DCOLRGVSTPMQEMLETASTLKGATDRSLTIDELGRGTSTYDGFGLAWAISETATV 775
 Db 716 DSQLRGVSTPMQEMLETASLRSATKDSLTIIDEGRGTSTYDGFGLAWAISETATV 775

QY 773 APLTFATHPEHETLANKNGDNGKKKAGIANFHVPAHIDPSNRKLTMLYKUHPGACDQS 832
 Db 776 AFCMFATHPEHETLANT-----QIPTVNNLHVITAL-TTEETLTMXQVKRGCVCDQS 825

QY 833 FGIVYAFANFPPSVVALLAREKASLEDSPESIALIPN-DIKEAASKR--KREFDRHDVS 888
 Db 826 FGIVYAEELANFPKHVIECAKQKALEBFQYIGESQGDIMEPAKKCYLERE----- 878

QY 889 RGATARARQFLQDPAOLPDKMDPNVVRQKLSKMKTDL 925
 Db 879 QGEKLIQEFLSKVKOMPTEEMSEENITIKLQLKAEV 915

QY 354 LDIVOSFVEDAALRQDIROH-LKRISDIERLTHNLERKASLYHVVVKLYQSSTRPVYIKS 412
 Db 360 LNIVEAFVDEAEROTLDRFLDNLREFFPDINRLACKFORQANLOCYRIOGQNOLPNVYI 419
 QY 413 VLERHDGQPATLERYIDSLEKNSDDNEHLNKFTGLVETSVDLQLENGEYIMISSAYDPN 472
 Db 420 ALECHEGHQKQLLAFLAVFTPLTDLRS - FSQFOEMIETLMDQVENHEFLYKPSFPDN 477
 QY 473 LSALJDKDEOFTLEROIHNHLKOTANDLDPIDSKSLKLDKETOFGHVFRITKEPKVRLQ 532
 Db 478 LSEIREMMDLEKQNSTLISAAARDLGQDGPQKILDSAAQFGYFVRVCKEYKLRN-- 535
 QY 533 NSHYTVLTERPKGVKFPTKLUKGDOFOKITVVERYSQKELYARVVCOTAASESEVEFGI 592
 Db 536 KNFNESTVDIOKGYKFTNERSLTTSNEEYTKNTKTYEEADQAVKEVINISSGIVBPMOTL 595
 QY 593 AGVLAELDVLSFDLAAASCPTPYTRPNISPDTGDIILEGRCPCEVAQDWINSIPNDIC 652
 Db 596 NDVLAQDAAVSPAHVNSGAPVYVPRALLEKGQGRILILKAARHACVEYQDELAIFPNDV 655
 QY 653 RLVRGESWSWFOITGENMGKKSTYERQVGTVNVLMAQGVFCPESEAEVSIVDCILARVGAG 715
 Db 656 YFERDKQMPFHITGPNNMGKKSTYERQGTIVNVLMAQGVFCPESEAEVSIVDCILARVGAG 715
 QY 713 DCQLRGVSPTMHOEMLETASTIKGATDRSLTIDELGRGTSTYDGFGLVAAICEHIVEEIK 772
 Db 716 DSQURGVSTPNAEMLETASTIRSATKDSLIIDEGRGTSTYDGFGLVAAISEYATKIG 775
 QY 773 APTLPATHFELTALANKDNGHKKNAGIANHNFYAHIDPSNRKLTMLYKVHGACDOS 832
 Db 776 AFCPMPATHFELTALAN----QIPTVNHLHYTALETEETLTMLYQVKKGVCQDGS 825
 QY 833 FG1HYAEAFANFPPSVVALAREKASELEDPSDIA1TPN-DIKEAASKR -- KREFDRHDV 888
 Db 826 FGTHYADELANPKHVICAKQKALEFLFQYGESESQGYDIMEPAAKCYLRE----- 878
 QY 889 RTATARARQFLQDFQAOLPLDKMDNPVNVRQKLSMKMTDL 925
 Db 879 QGEKTIQEFLSKVKQNPFTENSEENITIKQQLKAEV 915

RESULT 12
 ; Sequence 11, Application US/10243130
 ; Publication No. US20031143622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaides, Nicholas C.
 ; APPLICANT: Grasso, Luigi
 ; APPLICANT: Sass, Philip M.
 ; TITLE OF INVENTION: ANTIBODIES AND METHODS FOR GENERATING GENETICALLY ALTERED
 ; TITLE OF INVENTION: ANTIBODIES WITH HIGH AFFINITY
 ; FILE REFERENCE: MOR-130
 ; CURRENT APPLICATION NUMBER: US/10/243,130
 ; CURRENT FILING DATE: 2002-09-13
 ; PRIOR APPLICATION NUMBER: 09/707,468
 ; PRIOR FILING DATE: 2000-11-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 11
 ; LENGTH: 934
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-243-130-11

Query Match Score 37.9%; Score 1841.5%; DB 14; Length 934;
 Best Local Similarity 43.0%; Pred. No. 3.6e-149;
 Matches 403; Conservative 172; Mismatches 307; Indels 5; Gaps 19;

QY 14 JKIDAKOAQGFLSEFKETLKPDP-RAYLFEDRDYTTSHGDATIPLAETYHTTALRQG 72
 Db 9 IOLESAAEVGYFRRQQMPEKPTTFLFEDSFXTAHEGDAALLAREVTQGTVKYM 68
 Qy 73 NR-ADALSSVSVSRNMETIARDILLERMDRTLELYEGSGSN-----WRLVKSGTGN 124

RESULT 13
 US-10-371-857-5
 ; Sequence 5, Application US/10371857
 ; Publication No. US2003165468A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Grasso, Luigi
 ; APPLICANT: Nicolaides, Nicholas C.
 ; APPLICANT: Sass, Philip M.
 ; TITLE OF INVENTION: Regulated Vectors For Controlling DNA Hypermutability in
 ; Eukaryotic Cells
 ; FILE REFERENCE: FTO0004 US-MOR-0144
 ; CURRENT APPLICATION NUMBER: US/10/371,857
 ; CURRENT FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: 60/358,602
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 5
 LENGTH: 934
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-371-637-5

Query Match Score 37.9%; Score 1841.5%; DB 14; Length 934;
 Best Local Similarity 43.0%; Pred. No. 3 6e-149;
 Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

Qy 14 LKLDKAOQFGLEFFKTLPKDP-RAVRLFDRDYYTSHGDDATIAYTYHMTTALRQLG 72
 Db 9 LQLESAAEVGFRFQGMPEKPTTVRLFDQDFYTAHGDEALLAAREVKQGVTKIMG 68

Qy 73 NR_ADALSSVSYSRNMPETIARDILLERMTRDTELEYGGSN-----WRLYKSGTPGN 124
 Db 69 PAGAKNQSVVLSKMNPFSEFKOULLVQQR-VEVYKTRAGKASKENDWLYAKSPGN 127

Qy 125 LGSEFDILFANNEMONSVAIAALPNFGCNGCEVGLGRVDITKRVLGTEFLDDSHFTNL 184
 Db 128 ISOFEDILFGNDMMSAISGUVGKMSAVDGQRQVGVGTVDSORKLGCLCEFPDNDQFSNL 187

Qy 185 ESalVALGCRECLVP-AET-GKSSSEYRPMDAITSRCGYMWTERKKTEFKGRDLVODIGRL 242
 Db 188 EAIIQJGPKECVLPGGETAGDNGKLROI---IQRGGLITERKADEFSTRDIYQDINRL 244

Qy 243 VKG-----SVEPVRLVSGFECASGAIGLISYAEELADESNYGNYTQYQNLNSYM 294
 Db 245 LICKRKGEOMNSAVLPME---NOVAYASVLSAVKFGLLSDNSNFQGFEFTDFDQYM 300

Qy 295 RLDSAMERALNVM-SKS DANAKNFSLFLGMNRTCTAGMGRKLIHLMKOPLADVEEINCR 353
 Db 301 KLDIAVRALNLLFGSVEDTTGSOSLLALINK-CKTPQGQLVNQMKOPLMKDKNRTEER 359

Qy 354 LDIVOSFYEDAALRDLRHOH-LKRISDIERLTHNLERKASLYHVKVLYOSSTRTRYPKS 412
 Db 360 LNLFYEAFADEAERQTLQDLRERPDINLRACKFORANLQDCYRXYQGINOLPNTIQ 419

Qy 413 VLERHDQGPFATLERYRIDSLSLEKMSDDNHLNKPIGLUBTSVLDQLENGEYMISSAYDPN 472
 Db 420 ALEXHEGHQKLLAVAFPLTDLRSD--FSKQEMITLMLMDOVENHEFFYKPSDPN 477

Qy 473 LSALKDQEFTLEROIHNLLHQKQTLNDLPIDKSLKLDKETOFHSEVERLTKEPKVKQL 532
 Db 478 LSELREIMDLKMQSTLISAAARDLGDPKQIKLSSAQFGYFVRTCKEEKVLRN- 535

Qy 533 NSHYTIVLETROGVKFTYTKLKLGQDFQRTVEYKSCOKELYARVYOTAASEFVPGI 592
 Db 536 NKRFSTVDIOLQNGKFTMSKLTSLNEETKNTKEYBEAOQDAIVKEVINISSGTVPEMOTL 595

Qy 593 AGVIAELDYLISFLADLAASCPTPYTRNPISPPDTGDLLEGCRHPCEVAQDNWNSIPNDC 652
 Db 596 NDYLAQDVAHNSVNGAPVPRPALEKSGGRITLKAHSACVQDEAFTIPRDV 655

Qy 653 RLVRGESWFOIITCPNMGSKSTYIIRQGYVNMLAQVGSEPVPCDNATISIRDCIFARYGAG 712
 Db 656 YFEKDKomPHIITCPNMGSKSTYIROTGYVNLAQIGCVPCESEAESTVDCCLARYGAG 715

Qy 713 DCQORGVSTMQEMBLETASILKGATDRSLJLIDBLGRGTSTYDGFGLAWAISEVIATKIG 772
 Db 716 DSQLGKVSTPMMAEMLETASILRSATKDSLIIIDBLGRGTSTYDGFGLAWAISEVIATKIG 775

Qy 773 APTLFATHFELTALANKNDGHHKKGAGIANFHVFHAIDPSNRKLTMLYKXHPGACDQS 832
 Db 776 AFCMPATHEFETALAN-----QIPPNVLNLVATL-TTEETLMLYQVKGVCQDQS 825

Qy 833 FGIVHAEEFANFPVVALAREKASELEDSPIALIPN-DIKEASKR--KRFDRHDVS 888
 Db 826 FGIVHAELANFPKIEVIECAKQKALELEEFQYIGESQG'DIMEPAAKCYLERE----- 878

Qy 889 RGTRARAROFLODQAOLPLDKMDPENVYRQKLSRMKMTDL 925
 Db 879 QGEKITOBFLSKVQMBETMESENITIKLKLKAEV 915

RESULT 14
 US-10-371-634-9
 i Sequence 9, Application US/10371634
 i Publication No. US20030170895A1
 i APPLICANT: Morphore Inc.
 i APPLICANT: Grasso, Luigi
 i APPLICANT: Nicolaides, Nicholas C.
 i APPLICANT: Sass, Philip M.
 i TITLE OF INVENTION: Methods of Making Hypermutable Cells Using PMSR Homologs
 i CURRENT APPLICATION NUMBER: US10/371,634
 i CURRENT FILING DATE: 2003-02-21
 i PRIOR APPLICATION NUMBER: US10/371,634
 i NUMBER OF SEQ ID NOS: 48
 i PRIORITY DATE: 2002-02-21
 i SEQ ID NO 9
 i SOFTWARE: PatentIn version 3.2
 i LENGTH: 934
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i US-10-371-634-9

Query Match Score 37.9%; Score 1841.5%; DB 14; Length 934;
 Best Local Similarity 43.0%; Pred. No. 3 6e-149; Mismatches 307; Indels 55; Gaps 19;

Qy 14 LKLDKAOQFGLEFFKTLPKDP-RAVRLFDRDYYTSHGDDATIAYTYHMTTALRQLG 72
 Db 9 LQLESAAEVGFRFQGMPEKPTTVRLFDQDFYTAHGDEALLAAREVKQGVTKIMG 68

Qy 73 NR_ADALSSVSYSRNMPETIARDILLERMTRDTELEYGGSN-----WRLYKSGTPGN 124
 Db 69 PAGAKNQSVVLSKMNPFSEFKOULLVQQR-VEVYKTRAGKASKENDWLYAKSPGN 127

Qy 125 LGSEFDILFANNEMONSVAIAALPNFGCNGCEVGLGRVDITKRVLGTEFLDDSHFTNL 184
 Db 128 ISOFEDILFGNDMMSAISGUVGKMSAVDGQRQVGVGTVDSORKLGCLCEFPDNDQFSNL 187

Qy 185 ESalVALGCRECLVP-AET-GKSSSEYRPMDAITSRCGYMWTERKKTEFKGRDLVODIGRL 242
 Db 188 EAIIQJGPKECVLPGGETAGDNGKLROI---IQRGGLITERKADEFSTRDIYQDINRL 244

Qy 243 VKG-----SVEPVRLVSGFECASGAIGLISYAEELADESNYGNYTQYQNLNSYM 294
 Db 245 LICKRKGEOMNSAVLPME---NOVAYASVLSAVKFGLLSDNSNFQGFEFTDFDQYM 300

Qy 295 RLDSAMERALNVM-SKS DANAKNFSLFLGMNRTCTAGMGRKLIHLMKOPLADVEEINCR 353
 Db 301 KLDIAVRALNLLFGSVEDTTGSOSLLALINK-CKTPQGQLVNQMKOPLMKDKNRTEER 359

Qy 354 LDIVOSFYEDAALRDLRHOH-LKRISDIERLTHNLERKASLYHVKVLYOSSTRTRYPKS 412
 Db 360 LNLFYEAFADEAERQTLQDLRERPDINLRACKFORANLQDCYRXYQGINOLPNTIQ 419

Qy 413 VLERHDQGPFATLERYRIDSLSLEKMSDDNHLNKPIGLUBTSVLDQLENGEYMISSAYDPN 472
 Db 420 ALEXHEGHQKLLAVAFPLTDLRSD--FSKQEMITLMLMDOVENHEFFYKPSDPN 477

Qy 473 LSALKDQEFTLEROIHNLLHQKQTLNDLPIDKSLKLDKETOFHSEVERLTKEPKVKQL 532
 Db 478 LSELREIMDLKMQSTLISAAARDLGDPKQIKLSSAQFGYFVRTCKEEKVLRN- 535

Qy 533 NSHYTIVLETROGVKFTYTKLKLGQDFQRTVEYKSCOKELYARVYOTAASEFVPGI 592
 Db 536 NKRFSTVDIOLQNGKFTMSKLTSLNEETKNTKEYBEAOQDAIVKEVINISSGTVPEMOTL 595

Qy 593 AGVIAELDYLISFLADLAASCPTPYTRNPISPPDTGDLLEGCRHPCEVAQDNWNSIPNDC 652
 Db 596 NDYLAQDVAHNSVNGAPVPRPALEKSGGRITLKAHSACVQDEAFTIPRDV 655

Qy 653 RLVRGESWFOIITCPNMGSKSTYIIRQGYVNMLAQVGSEPVPCDNATISIRDCIFARYGAG 712
 Db 656 YFEKDKomPHIITCPNMGSKSTYIROTGYVNLAQIGCVPCESEAESTVDCCLARYGAG 715

Qy 713 DCQORGVSTMQEMBLETASILKGATDRSLJLIDBLGRGTSTYDGFGLAWAISEVIATKIG 772
 Db 716 DSQLGKVSTPMMAEMLETASILRSATKDSLIIIDBLGRGTSTYDGFGLAWAISEVIATKIG 775

Qy 773 APTLFATHFELTALANKNDGHHKKGAGIANFHVFHAIDPSNRKLTMLYKXHPGACDQS 832
 Db 776 AFCMPATHEFETALAN-----QIPPNVLNLVATL-TTEETLMLYQVKGVCQDQS 825

Qy 833 FGIVHAEEFANFPVVALAREKASELEDSPIALIPN-DIKEASKR--KRFDRHDVS 888
 Db 826 FGIVHAELANFPKIEVIECAKQKALELEEFQYIGESQG'DIMEPAAKCYLERE----- 878

Qy 889 RGTRARAROFLODQAOLPLDKMDPENVYRQKLSRMKMTDL 925
 Db 879 QGEKITOBFLSKVQMBETMESENITIKLKLKAEV 915

RESULT 14
 US-10-371-634-9
 i Sequence 9, Application US/10371634
 i Publication No. US20030170895A1
 i APPLICANT: Morphore Inc.
 i APPLICANT: Grasso, Luigi
 i APPLICANT: Nicolaides, Nicholas C.
 i APPLICANT: Sass, Philip M.
 i TITLE OF INVENTION: Methods of Making Hypermutable Cells Using PMSR Homologs
 i CURRENT APPLICATION NUMBER: US10/371,634
 i CURRENT FILING DATE: 2003-02-21
 i PRIOR APPLICATION NUMBER: US10/371,634
 i NUMBER OF SEQ ID NOS: 48
 i PRIORITY DATE: 2002-02-21
 i SEQ ID NO 9
 i SOFTWARE: PatentIn version 3.2
 i LENGTH: 934
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i US-10-371-634-9

Query Match Score 37.9%; Score 1841.5%; DB 14; Length 934;
 Best Local Similarity 43.0%; Pred. No. 3 6e-149; Mismatches 307; Indels 55; Gaps 19;

Qy 14 LKLDKAOQFGLEFFKTLPKDP-RAVRLFDRDYYTSHGDDATIAYTYHMTTALRQLG 72
 Db 9 LQLESAAEVGFRFQGMPEKPTTVRLFDQDFYTAHGDEALLAAREVKQGVTKIMG 68

Qy 73 NR_ADALSSVSYSRNMPETIARDILLERMTRDTELEYGGSN-----WRLYKSGTPGN 124
 Db 69 PAGAKNQSVVLSKMNPFSEFKOULLVQQR-VEVYKTRAGKASKENDWLYAKSPGN 127

Qy 125 LGSEFDILFANNEMONSVAIAALPNFGCNGCEVGLGRVDITKRVLGTEFLDDSHFTNL 184
 Db 128 ISOFEDILFGNDMMSAISGUVGKMSAVDGQRQVGVGTVDSORKLGCLCEFPDNDQFSNL 187

Qy 185 ESalVALGCRECLVP-AET-GKSSSEYRPMDAITSRCGYMWTERKKTEFKGRDLVODIGRL 242
 Db 188 EAIIQJGPKECVLPGGETAGDNGKLROI---IQRGGLITERKADEFSTRDIYQDINRL 244

Qy 243 VKG-----SVEPVRLVSGFECASGAIGLISYAEELADESNYGNYTQYQNLNSYM 294
 Db 245 LICKRKGEOMNSAVLPME---NOVAYASVLSAVKFGLLSDNSNFQGFEFTDFDQYM 300

Qy 295 RLDSAMERALNVM-SKS DANAKNFSLFLGMNRTCTAGMGRKLIHLMKOPLADVEEINCR 353
 Db 301 KLDIAVRALNLLFGSVEDTTGSOSLLALINK-CKTPQGQLVNQMKOPLMKDKNRTEER 359

Qy 354 LDIVOSFYEDAALRDLRHOH-LKRISDIERLTHNLERKASLYHVKVLYOSSTRTRYPKS 412
 Db 360 LNLFYEAFADEAERQTLQDLRERPDINLRACKFORANLQDCYRXYQGINOLPNTIQ 419

Qy 413 VKG-----SVEPVRLVSGFECASGAIGLISYAEELADESNYGNYTQYQNLNSYM 294
 Db 413 VLERHDQGPFATLERYRIDSLSLEKMSDDNHLNKPIGLUBTSVLDQLENGEYMISSAYDPN 472
 Db 413 VLERHDQGPFATLERYRIDSLSLEKMSDDNHLNKPIGLUBTSVLDQLENGEYMISSAYDPN 472

Qy 454 LDIVOSFYEDAALRDLRHOH-LKRISDIERLTHNLERKASLYHVKVLYOSSTRTRYPKS 412
 Db 454 LDIVOSFYEDAALRDLRHOH-LKRISDIERLTHNLERKASLYHVKVLYOSSTRTRYPKS 412

Qy 473 LSALKDQEFTLEROIHNLLHQKQTLNDLPIDKSLKLDKETOFHSEVERLTKEPKVKQL 532
 Db 473 LSALKDQEFTLEROIHNLLHQKQTLNDLPIDKSLKLDKETOFHSEVERLTKEPKVKQL 532

Qy 533 NSHYTIVLETROGVKFTYTKLKLGQDFQRTVEYKSCOKELYARVYOTAASEFVPGI 592
 Db 536 NKRFSTVDIOLQNGKFTMSKLTSLNEETKNTKEYBEAOQDAIVKEVINISSGTVPEMOTL 595

Qy 593 AGVIAELDYLISFLADLAASCPTPYTRNPISPPDTGDLLEGCRHPCEVAQDNWNSIPNDC 652
 Db 596 NDYLAQDVAHNSVNGAPVPRPALEKSGGRITLKAHSACVQDEAFTIPRDV 655

Qy 653 RLVRGESWFOIITCPNMGSKSTYIIRQGYVNMLAQVGSEPVPCDNATISIRDCIFARYGAG 712
 Db 656 YFEKDKomPHIITCPNMGSKSTYIROTGYVNLAQIGCVPCESEAESTVDCCLARYGAG 715

Qy 713 DCQORGVSTMQEMBLETASILKGATDRSLJLIDBLGRGTSTYDGFGLAWAISEVIATKIG 772
 Db 716 DSQLGKVSTPMMAEMLETASILRSATKDSLIIIDBLGRGTSTYDGFGLAWAISEVIATKIG 775

Qy 773 APTLFATHFELTALANKNDGHHKKGAGIANFHVFHAIDPSNRKLTMLYKXHPGACDQS 832
 Db 776 AFCMPATHEFETALAN-----QIPPNVLNLVATL-TTEETLMLYQVKGVCQDQS 825

Qy 833 FGIVHAEEFANFPVVALAREKASELEDSPIALIPN-DIKEASKR--KRFDRHDVS 888
 Db 826 FGIVHAELANFPKIEVIECAKQKALELEEFQYIGESQG'DIMEPAAKCYLERE----- 878

Query 593 AGVLAEDVILSFAIDLAASCPPTYTRPNISPDTGDILEGCRHPCVBAQDWNNSIPNDC 652
 Database 596 NDVLAQDVALNSPAPVSYAANGAVPVYRPALEKGGRITLKAASHACVEVQDEAFIIPDV 655
 Query 653 RLVRGEBSWFOITGPNGMGKSTYIIRQVGNVNLMAQVGSPVCDNATISIRDCLFARVAG 712
 Database 656 YEEKDQMFHITGPNGMGKSTYIIRQVGVTLMAQIGCPVCEAEVSIVDCILARYAG 715
 Query 713 DCQLRGVSTMQEMLETASILKGANDRSIJIIDELGRGFTSTYDGFGLAWAIChIVERIK 772
 Database 716 DSQLGKVSTIFMAMMLETASILRSATKDSLIIIDEIGRTSTYDGFGLAWAISEVIAKIG 775
 Query 773 APTLFATHPELTALANKNGKKNAGTAENFHVAIHIDPSNRKLTMLYKTHPGACDQS 832
 Database 776 AFCPMFATHPELTALAN-----QIPIVNLNLTVALT-TTEETTLTMYQVKRGVCDQS 825
 Query 833 FGIVHAEPANFPSPVVALAREKASBLEDSPIALIPN-DIKEAASKR---KREDFRDHS 888
 Database 826 FGIVHAELLNFNPKPVIECAKQKALEEFEQYIGESQGVIMPEAKKCYLERE----- 878
 Query 889 RGTARARQFLQDFAQPLDRMDPNVVRQLSKMTDL 925
 Database 879 QGEKIQEFLSKVUOMPFTMSEENITIKLQLKAEV 915

RESULT 15
 US-10-348-074-7
 / Sequence 7, Application US/10348074
 / Publication No. US20030176386A1
 / GENERAL INFORMATION:
 / APPLICANT: Morphotek Inc.
 / APPLICANT: Grasso, Luigi
 / APPLICANT: Kline, J. Bradford
 / APPLICANT: Nicolaides, Nicholas C.
 / APPLICANT: Sass, Philip N.
 / TITLE OF INVENTION: Method for Generating Engineered Cells for Locus Specific Gene
 / FILE REFERENCE: MG0003 US (MOR-0140)
 / CURRENT APPLICATION NUMBER: US/10/348,074
 / CURRENT FILING DATE: 2003-01-17
 / PRIOR APPLICATION NUMBER: 60/349,565
 / PRIOR FILING DATE: 2002-01-18
 / NUMBER OF SEQ ID NOS: 47
 / SOFTWARE: Patentin version 3.2
 / SEQ ID NO 7
 / LENGTH: 934
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / US-10-348-074-7

Query Match 37.9%; Score 1841.5; DB 14; Length 934;
 Best Local Similarity 43.0%; Pred. No. 3.6e-149;
 Matches 403; Conservative 172; Mismatches 307; Indels 55; Gaps 19;

Query 14 IRLDAKQAQGTLSSFFTPLPDP-RAVRLFDQDYYTSHGDDATIATYYHTTALRQG 72
 Database 9 IQLESAAEVGFRVRFQGMPEKPTTVRLFDGYTAHKGEDALLAAREVFKTGVIKMG 68
 Query 73 NR-ADALSSVSVRMNFETIARDILLERMDTLEYEGSGSN-----WRLVKS GTPGN 124
 Database 69 PAGAKNLQSYTSLKONFESPWTKDILVRQR-VETYKKNRAGKASKENDWLYAKASPGN 127
 Query 125 LGSFEDILFANEMMNSPVTALAALPNFGONGCEVGLGYDITKRVGLTTEFLDDSHFTNL 184
 Database 128 LSQFEDILFGNNDMSASITGIVGVKNSAVIDGCRQVSYGVDSIQRKLGLCEPFDNDQFSNL 187
 Query 185 ESALVALGCRCLVP-AET-GKSSEYRPMFAISRCGVWMTVERKTEFGRDLYQDLGRL 242
 Database 188 EALLIQIGPKCVCVLFQGETACDMGKLKRQI---IQRGGILITERKKADFSTKDIYDNLRL 244
 Query 243 VKG-----SVEPVRDLYSGFECASGALCILSYAELLADESNTGNNTVKOYNLNSTM 294
 Database 245 LKGKKGBOANSAVLPEME---NOVAVSSLSSAVKFLLELSDFGSQFELTTEDFSQTM 300

Search completed: April 7, 2004, 10:52:31.
 Job time : 56 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	420.8	13.9	2805	4	US-09-651-656-4
2	420.8	13.9	2805	4	US-09-650-855-4
3	420.8	13.9	2947	1	US-08-457-176-1
4	420.8	13.9	2947	1	US-08-457-175-8
5	420.8	13.9	2947	4	US-09-220-132-8
6	420.8	13.9	3145	4	US-09-708-201-4
7	420.8	13.9	3145	4	US-09-788-657-9
8	335.8	11.0	3823	4	US-09-512-150C-1
9	234.4	7.7	723	4	US-09-651-656-2
10	234.4	7.7	723	4	US-09-650-855-2
c	136.8	4.5	3159	4	US-08-956-171B-231
11	135.8	4.5	3754	2	US-08-743-63-08
12	135.8	4.5	3754	3	US-08-526-840B-31
13	135.8	4.5	7760	4	US-08-961-527-63
14	135.8	4.5	2625	4	US-09-543-681A-2786
c	131.8	4.3	1230025	4	US-09-138-452A-1
15	122.2	4.0	1830121	4	US-09-790-98B-1
16	122.2	4.0	1830121	4	US-09-139-84A-1
17	122.2	4.2	2676	4	US-09-134-001C-2076
18	124.8	4.1	2676	4	US-09-328-352-2511
19	122.6	4.0	2658	4	US-09-107-532A-1450
20	122.2	4.0	2568	4	US-09-489-039A-2980
c	122.2	4.0	640681	4	US-09-790-98B-1
21	122.2	4.0	1830121	4	US-09-557-84A-1
22	122.2	4.0	1830121	4	US-09-643-90A-1
23	122.2	4.0	2577	4	US-09-134-001C-2023
24	121.4	4.0	2568	2	US-09-134-001C-2023
25	120.6	4.0	2568	3	US-08-468-558-1
26	120.6	4.0	2568	3	US-08-676-44A-1
27	106.3	3.5	3093	2	US-08-588-521-7

QY	719	GAGATTGGTACAGGATCTTGGTAGGCTCGTCAAGGGTTCA-----GTAGAAC 766	Db	1784 TGTGGAGGTATAGCTGGTACTCTGAGTTGGATGTTACTAGTGTGTTGCATT 1.843
Db	704	AAGACATTATCAGACCTCAACGGTGTGGAAAGGCAAAGGAGATGATA 763	Db	1772 CAAAGCAACACTCAANATGTTGTTACTTCAGCTAATGCTTGTGCTTGCACG 1.931
QY	767	CCTTCGAGATTGGTCTCTGGTTGATGTCATCGGGCTTGGGTCATACTTT 826	Db	1844 TGCTGCAGATGCCAACTCCCTACAAAGCCAATATCAGTCAGCAGATACAGG 1.903
Db	764	GTGCTGTATTGCCGAAATGGAGATCACGTTCACTCTGCGGTAAATCA 823	Db	1832 TGTCAAATGGCCGCTTCATATGACGACGATTTGGAAAGAACAAAGAA 1.891
QY	827	CTTATGCGAACTACTTGGGATGAGGAACATGGAACTACATCAACAATACA 886	Db	1904 ATATTATCTGAGGGTGTAGGCATCTCTGGCATCTCTGGGAAAGCTCAAGATTGGCTTAACCTCA 1.963
Db	824	AGTTTGTGACCTCTTACAGAATTCACCTTGACACTGACTACTTTG 883	Db	1832 GAAATTATTAAGATCCACGCTGTTGAGTTGAGATGAAATTGCAATT 1.951
QY	887	ACCTCAATAGTACATGAGATAGATTCTGCTGTATGAGGCAGTATGGAGA 946	Db	1964 TGCCTAACTGACTGTAGACTTAGTGGAGAGAGTGTCTGAGATATCACAGGCTTA 2.023
Db	884	ACTTCAGCCAGATATGAAATTGATATGAGGAGTCAAGCTAACCTTTAGG 943	Db	1952 TTCCCTTAAGGACCTATACCTTGGAAAGATGAAATTAACAGATTTCCACATTTACTGGCCCA 2011
QY	947	GRAAATCAGATGCTAAATAAAATTAGTGGTCTGTGATGAATAAGAACGTTGACTG 1006	Db	1952 ACATGGGGAAAGTCCACCTACATTGGCAGGTGTTGATGTTGCCTGATG 2.083
Db	944	GTTCGTGAAAGATAACCCTGGCTCTCACTCTGGCTGCCCTGCTGAATAAGTAAAA 1.003	Db	2012 ATATGGGGTAATACACATATATICGACAAACTGGGTGATACTACTATGCCCCAA 2071
QY	1007	CTGGAACTGGTAAAGGTATTGACACAGTGGCTGACACCTTTACTAGATGTAAG 1.066	Db	2084 TGGCTCTTTTGTCCATGGTACAAATGCTTCTATTCTGTTGATGTTGCTC 2.143
Db	1004	CCCTCTCAAGGAAAGAACACTGTTAACCTGGATAAGACA 1.063	Db	2072 TGGGTGTTGGCTTACATGTTGCAATGTCATGCTTACCC 2.131
QY	1067	AGATTAACCTGAACTGGCTGGATTACTTCAATCATCTGTTGAGGATGCTCGCTTGCCRAAG 1.126	Db	2144 GTGTTGGCTGGAGATGCCAGCTGAGGGTTCTACCTTATGCAAGAGATGTTG 2.203
Db	1064	GAATAGAGGAGCAT---CTGAAAGAAATTCTGAGATTGTTGAGGCTTGTGAAATGCAATGCGCA 1.123	Db	2132 GACTAGGGCTGCTGATCTGAAAGGAGCTACTGATAGATATTGATTGAGTTGTTG 2.191
QY	1127	ATTGAGGGAGCAT---CTGAAAGAAATTCTGAGATTGTTGAGGCTTGTGAACTACATCTG 1.183	Db	2204 AGACTGCTGATCTGAGCTTCACTGGCTGATGAAAGGAGTGTGCAATGTTG 2.263
Db	1124	CTTACAAAGAAATTACCTCTGAGTCCAGCTCAACCACTTCAGAAGTTC 1.183	Db	2192 AAATCTGCTCTATCTCTGCTGAACTGATTAATCATAGTGTGTTG 2.251
QY	1184	AGGGAAAGAGCCAGTTAGTGCACGTTGATTAACCTCTATGCTGACACAACTCTG 1.243	Db	2264 GCGGTGGGACATCAACCTACAGATGGCTTGGTTAGCTGGCTATTGTGAGCACATG 2.323
Db	1184	AAAGACAACCGCAAACTTACAAAGTCTTACCCGACTCTTACAGGTTAAACTAC 1.243	Db	2252 GAAGAGGAACTTACCTACAGTGGATTGGTTAGATGGCTTATACAGATACTATG 2.311
QY	1244	CATAATCAAAATGTTGGAACTGTATGAGCAATTTCAGAACATCATCAGGAAA 1.303	Db	2324 TGAAGAAATTAAAGCACCAACATTGTTGCAACTCTGACTGCTGATTAG 2.383
Db	1244	CTAATGTTACAGGCTCTGGAAACACTGAAAGTCTGAGTAACTTGTGGCG 1.303	Db	2312 CAACAAACATTGCTGTTGGATGTTGCAACCCATTCTGAGACTTACGCTTGTG 2.371
QY	1304	GTTATATGCTCTCTAGAAATGGAGTGTGATAATCACCTGAAATAGTCTAGGGTC 1.363	Db	2314 CCACAAATGAGCATGAACTTGTGAAATTTCATGTTGCTT 2.443
Db	1304	TTCCTGIGACTCTCTACTGAAATTGAGTGTGATAATCACCTGAAATAGTCTAGGGTC 1.357	Db	2372 CCATCTCG-----ATACCACTGTTAATATCATGTCATGCA 2.407
QY	1364	TCTGGAAACTCTGTCGACCTGTCATCAACTGGAATGAAATCATGTTCTG 1.423	QY	2444 TTGACACATTGACCCCTCTAAATGCAAGCTACTATGCTTACAGGTTACCCAGGTG 2.503
Db	1358	TGATGAAACACTTGTGATGATGAACTCTGAAACCTGTTGAAACCTT 1.417	Db	2408 CAGCACTA-----CCACTGAGAGACCTTAACCTGTTATCGGTGAAAGGTG 2.461
QY	1424	CATATGACCAAAATTCTGCTGAAAGTGTGAACTGAGCAATGGGCAAACTC 1.483	QY	2504 CTGTGATCAGAGTTGTTGATTCATGTTGCAATTGCAACTTTCACCCAGGTG 2.563
Db	1418	CATTGATCTCAATCTCAGTAATGAACTGAGTGTGAACTGAGTGTGAACTG 1.477	Db	2462 TCCTGTGATCAAACCTTGTGATCTGAGCTGTTACCTCCCTAAAGCATGAA 2.521
QY	1484	ATAATTGCAACAAACACTGGCAATGATCTGATCTAATGATAAGTCACTAAC 1.543	QY	2564 TGCTCTGGCTAGAGAAAGGCAATCTGAGTTGGAGGATTCCTCTCTTATTGCCATAATTC 2.623
Db	1478	AGTCACATTAATAGTGCAGCCAGATCTGCTGACCTCTGGACCTGGCAACAGATTAAC 1.537	Db	2522 TAGATGTGCTAAACGAAAGCCCTGGAACTGACTTGTGAGCTTGTGAAATGCG 2.581
QY	1544	TAGATAAAAGAACACAATTGGACACCTTCAAGTACCAATTGAGAACGACCAAAAG 1.603	QY	2624 CAAATGAACTAAAGGCCAGCTCAAAACGAAAGGAAATTGAA 2.669
Db	1538	TGGATTCCAGTGCAGATTGATTAATCTCTGTAACCTGTAAGGAAAGATGCC 1.597	Db	2582 AAGGATATGATCATGGAAACCAAGGCCAGCTCAAAACGAAAGTGTATCTGGA 2.627
QY	1604	TCAGAAAGCNCCTAAATCTCACTACATGTTCTGAAACCTAAGGATGGTAAAGT 1.663	RESULT 2	US-09-650-855-4
Db	1598	TTCGTA-----CHATAAAACCTTGTGACTGATGATTCAGAAAGATGGCTTAAT 1.651	i	Application US/09650855
QY	1664	TCACTATAACAAACTGCCCATTGATCTGATCTAATGATAAGTCACTAAC 1.723	i	Patent No. 636535
Db	1652	TACCAACAGCAAAATTGACTCTTCAATGAAAGTATACAAACAGAAATG 1.711	i	GENERAL INFORMATION
QY	1724	AAAGCTGTGCAAGAAAGATTGGTAGTCGTTGACTTCTCCGAGG 1.783	i	APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY
Db	1712	AGAAAGCCAGATGCCATTGCAATATTGCAATGAAATTGCAATG 1.771	i	CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
QY			i	TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
Db			i	FILE REFERENCE: IL-10284
			i	CURRENT APPLICATION NUMBER: US/09/650,855

;	CURRENT FILING DATE:	2000-08-29	Db	1184	AAAGACRAGCAGCAAACCTACAGATTGTTACCGACTCTATGAGGTATAATCAACTAC	1243	
;	PRIOR APPLICATION NUMBER:	60/192,764	Qy	1244	CATATTCAAAAGTGTGTTGGACGTCTAGTGGGAACTTCACATGGAAA	1303	
;	PRIOR FILING DATE:	2000-03-28	Db	1244	CTAATGTTATACAGGTCTGGAAAACATGAAGGAAATTATGTTGGCAG	1303	
;	NUMBER OF SEQ ID NOS:	106	Qy	1304	GTTATATTGATTCAGAGAAATGGGTGATGATAATCACCTGAATAAGTCTAGGTC	1363	
;	SOFTWARE:	PatentIn Ver. 2.1	Db	1304	TTTTTGAACTCTTACTCTTACTGATGTTGACCTTCTGTTCTCCAGTTTCAGAAA	1357	
;	SEQ ID NO:	4	Db	1304	TTTTTGAACTCTTACTCTTACTGATGTTGACCTTCTGTTCTCCAGTTTCAGAAA	1357	
;	LENGTH:	2805	Qy	1364	TTGTGGAAACTCTGTTGACCTTGTCACTTGAGATTGAGAAATCATGATTTCCTG	1423	
;	TYPE:	DNA	Db	1358	TGATGAAACACTTGTAGATGGTAAACCTGGTAAACATGAAATTCTTGAAACCTT	1417	
;	ORGANISM:	Homo sapiens	Db	1358	TGATGAAACACTTGTAGATGGTAAACCTGGTAAACATGAAATTCTTGAAACCTT	1417	
US-09-650-855-4	Query Match	13.9%	Score	420.8	DB 4; Length 2805;		
Best Local Similarity	51.3%	Pred. No.	6.4e-117	Indels	60; Gaps	7;	
Matches 1194; Conservative	0;	Mismatches	1072;				
Qy	359	ACTGGAACTGGTAAGTGGAAACCCAGGAATCTGGAAATTGAGGTATTCTGT	418	Qy	1424	CATATGCCAAATTATCTGTCGAAGGTGAGGAGAACATGGGACAAATTC	1493
Db	347	ATTTGGTATTGGCATATAGGGCTTCCTGGGAACTCTCTCACTGTTGAAGCACATCTCT	406	Db	1418	CATTGATCCPRAATCTCAGTGGATTAGAGAAATAATGAACTCTGGAAAGATG	1477
Qy	419	TTCCTAATAATGAAATGCAAATTCTCGGTGATTGCTCTGGCTCCAACACTCGCTC	478	Qy	1484	ATAATTGACAACAAACTGCCAATGCTGTTGATCTAATGTAATGTCACTAAC	1543
Db	407	TGGTAACATATGATATGTCAGCTCCTGGTTAAATGTCGGCTGT	466	Db	1478	RGTCAAGCTTAAATGATGCGCAGAGATCTGGCTGGAAACAGATPAAAC	1537
Qy	479	AGATGGATGAGTGGAGTGGCTAGGTATGTTGATAATACAGAGAGTCCTGGTTAA	538	Qy	1544	TGATTAAGAAACACATTTGGACACCTCTGAGACCTTCAGAAATTACAGAAGA	1603
Db	467	ATGCCAGAGAAGGTTGGATGGTGGATGTTGAGTGGAACTAGGACTGT	526	Db	1538	TGGATTCAGTCAGTGCACAGTTGGATATACTCTGTTGAACTGTAGGAA	1597
Qy	539	CGAATTCTCAGTGTAGCCACTTCACAAATTGGTCTGCTTGGTCTGCGT	598	Qy	1604	TCGGAAGCAGCTTAATTCTCAGTACATTTCTGAAACAGCTGAGTGGGTTAA	1663
Db	527	GTGAATTCCCTGTAATGATCATTCTCCAACTCTGGGCTTCATCCGATGGAC	586	Db	1598	TTCTGTA-----CAATAAAACTTGTAGATGATGTTGTTAAATGTTAAAT	1651
Qy	599	GGAGAGATGTCCTGTGACCGGGAGACTGGAAATCAGGCTATGTTG	658	Qy	1664	TCACCTATACAAACTCAAACACTGGAGATCAGPTCAGAGATGTTAGGGACTA	1723
Db	587	CAAGGGATGTTACCGGAG--GAGAGACTGTCGGAACATGGGAACTAGAC	643	Db	1652	TTACCAACGGAAATIGCTTAAATGAGATACTCCTAAATAAAACAGATAA	1711
Qy	659	ATGCAATATCTCAGTGTAGCTGGTACTGAAAGGAAACTGTAATTAAAGGA	718	Qy	1724	AAAGCTCTAGAAAGATTTGGTAGCTGTTGAGTCAAAACACTGCTGCA	1783
Db	644	AGATAATCAAGAGGGAAATCTGATCACAGAAAGAAAAGTCACPTTCRCAA	703	Db	1712	AGAAGGCCAGATGGCTATGCAATTATGTCATAATTCTCTGGCTATGAA	1771
Qy	719	GAGATTGGTAGGAACTGGCTGATGGTCTGGTAGGTTCACTGTTGAGGTC	66	Qy	1784	TGTTTGGCACTAGCTGTTGCTGTTACTGCTGAGTTGGATGTTGCTGATT	1843
Db	704	AGACACATTATGAGGCTCAACGGGTGTTGAAAGGAGCCGAGATGATA	63	Db	1772	CAATGCGGAGACTCTAATGATGNTGTTGCTAGTGTGCTGTTGCA	1831
Qy	767	CGTTCTGGATTTGTTCTGGTTGCAATGGTCATGGCCCTTGGTCATACCTT	826	Qy	1844	TGGTGCCTGGCCACTCCCTACACAACTATGTCATATTCTCTGGCTATGAA	1903
Db	764	GTGCTGATTGGCAAATGGGAATGGTCACTGCTGTTGAGGAGAGTGGAA	823	Db	1832	TGTCATTGGACCCCTGTCATATGACGCCGCAATTGGAAAGGACACGAA	1891
Qy	827	CTTATGCCGAAACTACTCTGGGAGGCAACTATGCAACAAATACA	886	Qy	1904	ATATTATACTGAAAGGCTGAGCTTGTGAAAGCTTGTGAACTCTCA	1963
Db	824	AGTTTTAGAACCTCTTACAGTGAATTGGATATGGCTGAACTCTTGTG	883	Db	1892	GAATTATTAAGGCTCCAGGCTGTTGTTGAAGTCAAGTAAATTGCA	1951
Qy	947	GCAATCAGATGCTAATAAATTTAGCTTCTGCTGTTGAACTGTCATCT	1006	Qy	1964	TCCCTATAGCTGTTGAGCTTGTAGCTGTTGAGGAGTTCTCAGAGGCTA	2023
Db	944	CTTCCTGTAATACTGGCTCTGCTCTGGCTCTGGCTGAAATAGTGAAA	1003	Db	1952	TCCTCATGCTATCTTGTGAAAGATAACAGTGTTCACATGTTGCTGCA	2011
Qy	1007	CTTGAATGGTAAAGGTATTGTCATGTCAGCTGCTGAGCAACCTTACTA	1066	Qy	2024	ACATGGCTGAAAGTGCACATTCGGGAGCTTGTGTTGCTGTTGCAAG	2083
Db	1004	CCCCTCAAGGAAAGCTTACCTGTTGAACTGGCTCTCATGTTAAGAAC	1063	Qy	2014	GTGTTGGCTGGAGATTGCCAGTCAGGCTGAGGAGTTCTACATGGCCAA	2071
Qy	1067	AGTTAATGGTGTGAAATTGTCATCTGGCTGTTGAGGAGTTGGGCA	1126	Qy	2084	TTGGCTGTTGTTGCTGATGTTGAGCTTCTGTTGTTGATGTTGCTC	2143
Db	1054	GTATAGGGAGAGATGTTAGTGGCTGTTGAGGCTTGTGAACTGTTG	1123	Db	2072	TGGGTGTTGCTGCACTGAGTGTGCTGTTGCACTGTTGCTGTTG	2131
Qy	1127	ATTGAGCCGAT---CTGAAAGAATTTCGATATTGAGGGCTAACACAACTTG	1183	Qy	2204	AGACTGCTGATGTTGAGCTGTTGAGCTGTTGAGCTGTTGAGTGG	2263
Db	1124	CTTACAGAAGAATTCTGGTAACTCTGGCTGTTGAGGCTAACACAACTTG	1183	Db	2192	AAACTGCTGTTGCTGCTGAACTGAGATTCATGTTGAGTGGTGG	2251
Qy	1184	AGGAAAGAGGCAAGTCTACCTACAGTCAAGTACAGAGTAC	1243	Qy	2264	GCCGTGGACATCAACCTACATGGTTGTTGAGCTGCTTACATG	2323
Db	2252	GAAGAGGAACTCTACCTACAGTCAAGTACAGTCAAGTACATG	2311	Db	2252	GGGTGGTACCTACAGTCAAGTACAGTCAAGTACATG	2311

RESULT 3
US-08-457-176-1

Sequence 1, Application US/08457176
Patent No. 5591826

GENERAL INFORMATION:

APPLICANT: Vogelstein, Bert
Kinzler, Kenneth W.
de la Chapelle, Albert

TITLE OF INVENTION: Mutator Gene and Hereditary
Polyposis Colorectal Cancer

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, Mickie, and Beckett
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457.176
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160295
FILING DATE: 02-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 01107.44900

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
TELEX: 197430 BBMB UT

SEQUENCE CHARACTERISTICS:
SEQUENCE FOR SEQ ID NO: 1:
LENGTH: 2947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-457-176-1

Query Match 13.9%; Score 420.8; DB 1; Length 2947;
Best Local Similarity 51.3%; Pred. No. 6.6e-117; Mismatches 1072; Indels 60; Gaps 7;

Matches 1194; Conservative 0; ATCGGGAGACTGGTAAAGGGAAACCCAGGGAAATCTTGGGAACTTTGAGGATAATTCTGT 418
Qy 359 ATCGGGAGACTGGTAAAGGGAAACCCAGGGAAATCTTGGGAACTTTGAGGATAATTCTGT 418
Db 415 ATTGGPATTTGGCATATAAGCTTCCTGCCTCACTCTCAGTTGAAGAACATTCT 474
Qy 419 TTGCTTATAATGAAATGCCAATTCCTCGGTGATCTGGCTCTGTCACAACCTGGTC 478
Db 475 TTGGTACACATGATGTCAGCTTCAATGGTGTSTGGGTAAAATGTCGGTAGTTG 534
Qy 479 AGAATGGATGTAAGTGGCTTAGGGTATGTTGATTAAGAGAGTCCTGGTTAA 538
Db 535 ATGGCCAGAGCAGGTGGAGTGGATTCATAGGAAACTAGGACTG 594
Qy 539 CAGAAATTCTAGATGATGAACTTCAAAATTGGAGCTGCTGGCAATCCATGAAATGGGCTATGTTG 598
Db 595 GTGAATTCCCTGATAATGATCAGTTCCTCACTCTGAGGTCTCCATCCAGATGGAC 654
Qy 599 GCAGAGAAATGCTTGTACCGGGAGACTGGCAATCCATGAAATGGGCTATGTTG 658
Db 655 CAAAGGATGTTTGTACCCGAG--GGAGAGCTGCTGGGACATGGGAAACTGGAC 711
Qy 659 ATGCAATTCTAGATGGCTGTGACTGTAAGAAAGAAACTGTAAGGGA 718
Db 712 AGATAATTCAAGGAGGAATTCTGATCACAGAAGAAAAGCTGACTTTCCACAA 771
Qy 719 GAGATTGGTACAGGATCTTGTAGGCTCTCAAGGGTCA - - - - - GTAGAAC 766
Db 772 AAAGACATTATAAGGACCTCACACTTCACACTTGACATGACTACTTTG 951
Qy 767 CTGTTGAGATTGGCTCTGGTTGATGTCATCGGGCTTNGGNGCATACTT 826
Db 832 GTGCTGTATGGCAGAAATGGGAAATGGGTCAATCTGGGTATATCACTCTGGGTATACA 891
Qy 827 CTTATGAGAACTCTGGATGAGGAACTATGCAAAACATACA 886
Db 892 AGTTTTTAGAACTCTTATCAGTATGTCACATTGACATGACTACTTTG 951
Qy 887 ACCTCAATAGTACATGAGATTGAGGAACTTGTGCTATGAGGAACTGTTATGGGA 946
Db 952 ACTTCACCACTGATATGAAATTGGATATGGCTACCTTTTCAGG 1011
Qy 947 GCAAAATGAGATCTTAATAAAATTAGCTGTTGCTGTGATGAAATGAGCTGTACTG 1006
Db 1012 GTTCTGTGTTGAGATACCTGGCTCTGCTGCTGGCTGCTGGCTGCTGGCTGCAAG 1071
Qy 1007 CTGGAATGGTAAAGTTATGCAATGTGCTGAAACTCTATCAGTCAGTACAGTACAG 1066
Db 1072 CCCTCTAAGGCAAAAGACTTGTAAAGCTGCTCTCATGCTATAAGACA 1131
Qy 1067 AGATTAATGTAAGCTGATGTTAGTTGCAATCTGGATGTCATGTTG 1126
Db 1132 GATAGAGGAGGATCAATTAGTGGAAAGTGGATGAGATGAGGAAATGGGAGGA 1191
Qy 1127 ATTGGAGCCAGCT -- CTGAAAAGGATTCAGATATTGAGGCTGTCATGTTG 1183
Db 1192 CTTTACAGAAGATTTACTTCGATTCCCAGATTCGGCACTTCAGAAGTTTC 1251
Qy 1164 AGAGGAAAGAGCCAGTTAGTGCACGTTGAAACTCTATCAGTCAGTACAGTACAG 1243
Db 1252 AAAGACAAAGCAGCAAAACTTACAGATGTTACCGACTCTATCAGGSPATAATCAACTAC 1311
Qy 1244 CATATATAAAAGTGTGTTGAGCTGATGATGGCAACACAATCTG 1303
Db 1312 CTAATGTTATAAGGGCTCTGGAAAATGAGGAAACACCAAAATTATGTTGGCAG 1371
Qy 1304 GGTATATTGATTCCTAGAGAAATGGGGTGTGATGATAATCACCTGAAATAAGTICATAGTC 1363

1372 TTTTGTAACCTCTTACTGA-----TCTTCGACTCTCCAGTTCAAGAA 1425
 Db 2440 CCAATCAG-----ATACCPAATGTAAATAATCATGTCA 2475
 Qy 2444 TTGGCACATTGCCCTCTTAATGCAGCTAACTATCTTCAAGGTTAACCGAGTG 2503
 Db 2476 CAGCACTA-----CCCTGAGAGACCTTAACCT 2529
 Qy 2504 CTGTGATCAGAGTTGGTATTCATGTGCTGAATTGCAAAATTTCACCGAGTGTG 2563
 Db 2510 TCTGTGATCAGAGTTGGTATTCATGTGCTGAATTGCAAAATTCAACGTTAA 2589
 Qy 2564 TGGCTCTGCTGTAGAAAGGATCTGGTGGAGGATTTCCTCCATTGCTTAATTTC 2623
 Db 2590 TASAGTGCTAAACGAAGGCCCTGGAAATGCTGATATTCAGGATTTGGAAATGCG 2649

1364 TTGTGAAACTCTGGCTCACTGATCACTGAAATGGAATCATGTTCTTCTTCTG 1423
 Qy 1426 TGATGAAACAATTAGATGAACTTGTGAACTTGTGAAACATGTTCTTCTG 1485
 Qy 1424 CATATGCCAAATTATTCGCTCTGAACTGAGCAACATGGAGCACAATT 1483
 Db 1486 CATTGACCTTAATCTCAGTAACTGAAATTAATGATGACTGAAAGAGATG 1545
 Qy 1484 ATATTGGAACAAACAAACTGCCATGATCTGATCTACCTATGATAAGTCACTTAAC 1543
 Db 1546 AGTCAACATTAAATAGTGCAGCCAGATCTGGCTTGACCTGAAACAGATTARAC 1605
 Qy 1544 TAGATAAAAACAAACAAATTGGACACGCTCTTCAAAATGAAAGGACCAAAG 1603
 Db 1606 TGGATTCCAGTGCACAGTTGGATATTACTTCTGTAAACCTGTAACCTGAAAGGAAAGTGTCC 1665
 Qy 1604 TAGGAAGGAGCTAAATCTCACTACATGTTCTGAAACACCTAAGGATGGGTAAGT 1663
 Db 1666 TTGCTAA----CAATAAAACCTTGTACTGTAGATTCAGAGATGGTTAAAT 1719
 Qy 1664 TACCCCTACAAACCTAAACAAACTAGGAGATCAGTTCCAGAGAGTTGTAGGAGTCA 1723
 Db 1720 TTACCAACGAAATTGACTCTTAAATGAAAGTATACCAAAATAACAGAAATG 1779
 Qy 1724 AAAGCTGAGGAGAAAGAATGTTAGCTCTGTAAGTCAAAAGCTGGAGTTCTCCGAGG 1783
 Db 1780 AAGAGGCCAGATGCCATTGTTAAAGAAATGTCATAATTCTCAGCTTGTAGAAC 1839
 Qy 1784 TGTGTCAGGTTAGCTGTACTTGTGACTGTTGAGTTGTACTGAGTTTGCGGATT 1843
 Db 1840 CAATGCAAGCACTCAATGTTGTTAGCTCAGTCACTGTTGCTCG 1899
 Qy 1844 TGGTGCAGTGECCAACCTCCCTACAGACCAAAATPATCAGTCCACAGGAG 1903
 Db 1900 TTGTAATGGGACCTGTTCATATGTCAGGACCATTTGGAAAGGACAAGGA 1959
 Qy 1904 ATATTATACTTGGAGGCTTGGGATCCTTGTGGAAGCTCAGATGGTTAACCTCA 1963
 Db 1960 GAAATTAAAGCATCAGGCTATGGCTGTGAACTTCAGATGAATGCAATTAA 2019
 Qy 1964 TTCTTAATGACTGTAGACTTAGTTGGGAGAGACTGGTTCAAGTATCACAGGCCCTA 2023
 Db 2020 TTCTTAATGACTGTAGACTTGAAAGATAAACGATGTCACTCATCTGGCCCCA 2079
 Qy 2024 ACATGGGTGAAGTCACCTCAATTCGGCAGGTGGTGTGATGCCCAAG 2083
 Db 2080 ATATGGAGTAAATCAACATATTCGACAACAGTTGACTCATGCCAA 2139
 Qy 2084 TTGGCTGTGTTGCTCATGTGAACTGCAATTCGTTGATGTTGCT 2143
 Db 2140 TTGGGTGTTGCTCATGTGAACTGCAATTCGTTGATGTTGCT 2199
 Qy 2144 GTCTTGCCCTGGAGATGCCAGTCACTTCGTTGATGTTGCT 2203
 Db 2200 GAATGGGACTTCACTCTGGTGAACACTCAATTGAAAGGAGCTCTGGCATGTTG 2259
 Qy 2204 AGACTGATGATCTGAAAGGAGCTACTGATAATGATGAGTTGG 2263
 Db 2260 AACCTGCTCTATCTCAGTGTGAAACAAAGTTCAATCATGTAATGG 2319
 Qy 2264 GCCGGGGACATCACTCTGGTGAAGGAGCTCTGGCATGTTGCT 2323
 Db 2320 GAAGAGAACCTTACCTGAGTGTGATGTTGAGTGGCTATACATG 2379
 Qy 2324 TTGAAAGAAATTAAAGCACCACATGTTGCACTCACTTCACTGATGCTGATGCTAG 2383
 Db 2380 CAACAAAGATGGAGACAACTGGACATAAGAAAATGCGGGATGCAATTCTGCTGG 2439
 Qy 2384 CCACAAAGATGGAGACAACTGGACATAAGAAAATGCGGGATGCAATTCTGTT 2443

RESULT 4
 US-08-457-175-1
 Sequence 1, Application US/08457175
 Patent No. 5693470

GENERAL INFORMATION:
 APPLICANT: Vogelstein, Bert
 APPLICANT: Kinzler, Kenneth W.
 APPLICANT: de la Chapelle, Albert
 TITLE OF INVENTION: Mutator Gene and Hereditary
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner, Birch, McKie, and Beckett
 STREET: 1001 G Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20001

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/457,175
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/160295
 FILING DATE: 02-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107-44900
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEX: 197430 BBMB UT
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2947 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens

US-08-457-175-1

Query Match Score 420.8; DB 1; Length 2947;
 Best Local Similarity 51.3%; Pred. No. 6.6e-11; Indels 60; Gaps 7;

Matches 1194; Conservative 0; Mismatches 1072;

Qy	1424	CATATGACCCAAATTATCTGCTTGAGGTGAGCAAGAGAACATTGGGCCACAATT	1483	Qy	2504	CTTGTGATCAGAGTTGGTATTGATGCTGAATTGCAAAATTTCACCGAGTTG	2563
Db	1486	CATTGATCTTAACTCAGGATTAGAAGATAACTTGAAAGAAGATGC	1545	Db	2530	CTTGTGATCAGAGTTGGTATTGATGCTGAATTGCAAAATTTCACCGAGTTG	2589
Qy	1484	ATAATTGCAACAAACTGCCAATGATCTGATCACCTATTGATAAGTCACTTAAC	1543	Qy	2564	TGCGCTCTGGTAGAGAAAAGGATCTGAGTTGGAGGATTTCCTCTTATGCT	2623
Db	1546	ACTCAAATTAATAAGTGCAGCCAGAGATCTGGCTTGAGAACAGATAAAC	1605	Db	2590	TAGAGTGTGTAACAGAAAGCCCTGEAACTTGAGGAGTTCAAGTATGGAGAAT	2649
Qy	1544	TGATARAAGAACACAAATTGGACACGCTCTTCAAAATTACCGAAGAACAAAG	1603	Qy	2624	CAATAGCTTAAGRGAGCCTCARAACGAGAGAAATTG	2669
Db	1606	TGGATTCAGTSCACAGTTGGATATTACTTCTGTAACCTGTAACCTGAAAGTCC	1665	Db	2650	AAGGATATGATPATCAGAACAGAACAGAACAAAGTGTATCTGGA	2695
Qy	1604	TAGGAGCAGGTAATTCTCACTACATGTTCTGAAACACGCTAAAGTGGTAAAGT	1663		RESULT 7		
Db	1666	TTCGTTA-----CAATAAAACTTGTACTGTAGATCTGAGAAATGTTAAT	1719	US-09-788-657-9	Sequence 9, Application US/09788657		
Qy	1664	TGACCTATACAAACTCAAACAAACTAGGAGATCAGTTCCAGAAGATGTTGAGG	1723	PATENT NO.	6556736		
Db	1720	TACCAAAGCAAAATGACTCTTAAATGAGATAACCAAATAACAGAAATATG	1779	GENERAL INFORMATION:			
Qy	1724	AAAGGCTGTCAGAAGAAATTGGTAGCTGTTGAGTCTGAGCTGCTCGAGG	1783	APPLICANT: Nicolaides, Nicholas			
Db	1780	AGAAAGCCAGGATGCCATTGTAAAGAAATTGTCATAATTCTCTAGGGTATG	1839	APPLICANT: Sassi, Philip			
Qy	1784	TCTTGTGAGGTTAGTGTGFACTGCTGACTGTTGGATGTTGCGGATT	1843	APPLICANT: Kinzler, Kenneth			
Db	1840	CAATGCGAGACHTCAATGATGTTGTTGCTCACTAATGCTGTTGCTGAGC	1899	APPLICANT: Grassi, Luigi			
Qy	1844	TGGCTGCCAGTGCCTCAACTCCCTACAAAGCCAATAATGTCCTCCACAGG	1903	APPLICANT: Vogelstein, Bert			
Db	1900	TCTCAATTGGACGACCTGTCTCATATGTACGACGCAATTGGAAAGCAGGA	1959	TITLE OF INVENTION: Methods for generating hypermutable			
Qy	1904	ATATTATACTCGAGGTGTAGGCATCTTGTGAAAGTCAAGTAACTCCA	1963	TITLE OF INVENTION: yeast			
Db	1960	GGATTATTAAGACATCCAGGCACTCTGTGAGTCAAGTAAATGCAATTAA	2019	FILE REFERENCE: 01107.00097			
Qy	1964	TTCCTATGACTGTAGACTGTAGCTGTTGGAGAGAGTGTGTTGAACTTCA	2023	CURRENT APPLICATION NUMBER: US/09/788,657			
Db	2020	TTCCCTATGACCTTAACTTGTGAAAGATAALACAGATGTTCCACATCATTTG	2079	CURRENT FILING DATE: 2001-02-21			
Qy	2024	ACATGGGTGAAAGTCACCTACATGGCAGCTTGTGATGCTCTGGCCAAG	2083	PRIOR APPLICATION NUMBER: 60/184,336			
Db	2080	ATATGGCAAGTAAATCAACATATAATTGACAACACTGGTAAATGACGTTA	2139	PRIOR FILING DATE: 2000-02-23			
Qy	2084	TGGCTGCTTCTTCCATGTCGAATGCTTCACTTCTGTTGATTTGCTC	2143	NUMBER OF SEQ ID NOS: 25			
Db	2140	TGGGGTTGTTGCTGCACTGATGTTGCTGATGTTGCTGATCTAGGCC	2199	SEQ ID NO. 9			
Qy	2144	GTCCTGGCGTGGAGATTGCCGCTGAGATTTGCGTCTACTTTATGCAAG	2203	LENGTH: 3145			
Db	2200	GRTGAGTGTGCTGAAAGGAGTACTGATAGTCAATGTTGAGTTGG	2259	TYPE: DNA			
Qy	2204	AGACTGCTGATGTTCTGAAAGGAGTACTGATAGTCAATGTTGAGTTG	2263	ORGANISM: Homo sapiens			
Db	2260	AAACTGGTTCTCTCAGGTGCAACCAAGATCTTATCATAGTGAATTGG	2319	SEQ ID NO. 9			
Qy	2264	GCCTGGGACATCAACCTACGATGGCTTACCTGGCTGAGCATTTG	2323	LENGTH: 3145;			
Db	2320	GAAGAGAACTCTACATGGCTTACGATGTTGCTTACATGGCTTACAT	2379	Best Local Similarity: 51.3%; Pred. No. 6.9e-11; Mismatches: 0; Indels: 60; Gaps: 7;			
Qy	2324	TGAGAGAAATTAAAGGACCAACATGCTTGGCTTACGCTTACATGCT	2383	Matches 1194; Conservative: 0; Mismatches: 1072; Indels: 60; Gaps: 7;			
Db	2380	CAACAAAGATGTTGCTTACGCTTACATGGCTTACATGGCTTACAT	2439	Qy 359 ACTGGGACTGTGTTGAGTAAAGTGGAAACCAGGGAACTTGGAGGATTTGAGGATAATTCTGT	418		
Qy	2384	CAACAGAAATGGAGCAATGGACATAAGAAATTCTGGGATAGAAATT	2443	Db 415 ATTGTGATTTGGCATATAAGCTTCTGCAATTCTCAGTTTGAAGAACATTCT	474		
Db	2440	CGATCTG-----ATACCAACTTCAATCTACATGTCAGCTTCA	2475	Qy 419 TTGGCTTAAATGAAATGCAAAATTCTCCGGGATTTGCTCTGCTCAAAACTCTGGTC	478		
Qy	2444	TGGTACATGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2503	Db 475 TTGGCTTAAATGAAATGTCAGCTTCAATGTCAGCTTCAATGTCAGCTTCA	534		
Db	2507	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2529	Qy 479 AGAATGGATGTGAGTAACTGGCTTAGGTATTGATTAAGAGAGTCCTTGGTTAAATGTCAGCTTCA	538		
Qy	2527	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2573	Db 535 ATGGCAGAGACAGGTGGAGTTGGCTATGGTTCATAGGAAAAACTGAGAC	594		
Db	2573	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2619	Qy 539 CAGAATTCTGATGATGACACTTCACAAATTGGAGTTGCTTGTGCTTCTGAGTCA	598		
Qy	2619	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2663	Db 595 GTGAAATTCCCTGATATGATCAGTCACTTCATGTCAGTTCTCATCGAGTGGAC	654		
Db	2663	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2707	Qy 599 GCAGGAATGTCCTGCTACAGCTGCAAAATCAGTGAATACAGGCC	718		
Qy	2707	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2751	Db 659 ATGCAATATCTAGATGTCAGTCACTTCTGAGTCACTTCTGAGTCA	711		
Db	2751	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2795	Qy 659 ATGCAATATCTAGATGTCAGTCACTTCTGAGTCACTTCTGAGTCA	712		
Qy	2795	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2839	Db 712 AGATTTCAAGAGGGAATTCTGATACAGAAAAGCTGACTTTCAC	771		
Db	2839	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2883	Qy 719 GAGATTGGTACAGGATCTGGCTTACGAGTCACTTCTGAGTCA	771		
Qy	2883	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2927	Db 772 AAGACATTATCTGATGTCAGTCACTTCTGAGTCACTTCTGAGTCA	766		
Db	2927	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	2971	Qy 767 CTGTCGAAATTGGCTCTGGTCACTGAGTCACTGAGTCACTGAGTCA	831		
Qy	2971	GGTGGCTTCACTTCTGAGGTTACGAGTCAATTGAAAGTGG	3015	Db 832 GTGCTGTATTCGCCAGAAATTGGAGAACATCGGTATCATACTGTCGGTAA	891		

QY	827	CCTATGCGAAACTACTTGGGATGAGCAACTATGGAAACTDATACTACGTCAAACATAACA 86	Qy	1904	ATATTATACTTGAAAGGGTAGGGCATCCCTTGTTGGAAGCTCAAGATTGGGTTAACCTCA 1963
Db	892	AGTTTTAGAACCTCTTATCAGAAGTTCACCTTGGACAGTTGAACTTTTG 951	Db	1960	GAATTTAAAGGATCCAGGATTTGAACTTGAATTTGGAATTTGGAATTA 2019
QY	887	ACCTCAATAGTTACATGAGATACTGATGCTGCTATAGAGACACTGAAATGTTATGGAGA 946	Qy	1964	TTCCTTAATGACTGTAGACTTAACTTGGGAGAGAGTTGAGTTTCAGATTATCAACGGCCCTA 2023
Db	952	ACTTCAGCAGPATATGAAATTEGATATTGCAACGCCCTAACCTTTTCAGG 1011	Db	2020	TTCCTTAATGACTGTACTTCAAANGATAACAGATGTCACATCAACTGTGGCCCA 2079
QY	947	GCAATTCGATGTTAATAAAATTATTCAGTGAATAGAACTGTPACTG 1006	Qy	2024	ACATGGCTGAAAGTGCAGACCTACATTCGGCAATTCGGTGGGAATGTTCTGATGGCCCAAG 2083
Db	1012	GTTCCTGTGAAAGATAACATGGCTCTAGTCAGTCAGTCAGTCAGTAA 1071	Db	2080	ATATGGGAAATTAACACATAATTGCAAACTGGGATGATGACTCATGGCCCAA 2139
QY	1007	CTGGAAATGGTAAAGGTTATTCACATGTTGTTGAGCAACCTTACTAGTTAGAAG 1066	Qy	2084	TGGCTCTGTTGTCATGTTGAGTACATGTTGACATTCTATGTTGATTTTGTCT 2143
Db	1072	CCCTCAGGAAAGACTTGGATTTGTTAACCCTGTTAAGCAGGCTCTATGTTAGAAC 1131	Db	2140	TGGGTTGTTGTCAGTGAAGAGTTGCGAGCTGAGTGGCTTGTGCACTGGGTCAGCTAGCC 2199
QY	1067	AGATTAACCTGTAAGCTGGATTAGTTGTCATCATTTGCGAGGATGCGCTTCGCGCAAG 1126	Qy	2144	GTTGGCCGCTGGAGATGGAGGAGTTCACTTTATGCAASAGAGATGCTG 2203
Db	1132	GAACTAGGGAGGATGGATTGAAAGCTTGGAGCTTGTAGAAGATGGGARGA 1191	Db	2200	GAGTAGGGGCTGTGCACTGAAAGAGTCTCACGTCATGAAAGGTTGCTGAAATGTTGG 2259
QY	1127	ATTITGAGCCGAT - CTGAAGAAAATTTCGATATTGAGGGCTACACMACTCTG 1183	Qy	2204	AGACTGGCATCGATCTGTTGAAAGGAGCTACTGATAGATCATGGTATTGAGTTGG 2263
Db	1192	CTTACAGAAAGATTTACTTCGTCGATTTCCACAGTCACCTAACCGAGTTTC 1251	Db	2260	AAACTGTTCTPATCCMTCAGGCTGCAACAAAGATTCAATACTAGTGAATTTGG 2319
QY	1184	AGGGAAAGAGGGCAAGCTTGGACGTTAGTCACGTTGTTGAAACCTTACAGTCAAGTACAGACTAC 1243	Qy	2264	GGCGTGGGACATCAACACTACAGATGGCTTGTGCTGATTGAGCACATG 2323
Db	1252	AAGGAGGAGGAAACTTACAGATGTTGTTACCGACTCTATGGTATAATCAACTAC 1311	Db	2320	GRAGAGGAACCTCTACCTACGTTGGATTGCTGTTGAGCTTACATGGCTATACTAGTGAATATG 2379
QY	1244	CATATATCAAAAGTTGGAACTTGGCAATTTCGAAACACTCATCAGGGAAA 1303	Qy	2324	TGAAAGAAATTAAAGCACACATTTGCTGCACTTCACTGCTTGTGCTGATTGCTAGTTGG 2383
Db	1312	CTATGTTATACTGGCTCTGGAAAACATGAAGAAACACCGAAATTATTGTTGCCAG 1371	Db	2380	CAACAAAGATGTTGCTGTTGCTGATTTGCACTGAAACCCATTTCATGACTACTGCCTTGG 2439
QY	1304	GTATATGATGTTCTCTAGAAATGGAGTGTGATAATACTACCCGAAATTTAGTCAGTGGTC 1363	Qy	2384	CCACACAGAAATGGAGACATGGACATAAGAAAATGCTGGGATAGCAAAATTTCATGTT 2443
Db	1372	TCTTGTGTTGACTCTCTTACTGA-----TCTCTGTTGACTCTCCGTTACTGA 1425	Db	2440	CCAACTACG-----ATACAACTGTTAATACTCATGTTCA 2475
QY	1364	TGTGGAACACTCTGTTACCTTGATCACTTGAACTGTTGAACTGTTCTCTG 1423	Qy	2444	TGTCACACATTGACCCCTTCTAATCGCAGCTACTGTTTACAGGTTTACCCAGGTG 2503
Db	1426	TGATGAAACAACTTTAGATGATCGTGGGAAACCTGTTCTGAAACCTT 1485	Db	2476	CAGCACTCA-----CCATGAGAGACCTTAACTGTTTACAGGTTTACATGGTGAAGAAATG 2529
QY	1424	CATATGACCCAAATTATTATGCTGTGAGGATGAGCAGATGGGACAAATTTC 1483	Qy	2504	CTPTGTGATCAGAGTTGTTGGAATTTGCAATTTCACCGAGGTGTG 2563
Db	1486	CAATTGATCCTAACTCTAGTGAATTAGAGAAATAATGAACTGTTGAAACAGAATGTC 1545	Db	2530	TCTGTGATCAAAGTTGGATTGCTGAGGCTTGCCTAAAGCATTTAA 2589
QY	1484	ATATTTCGACAAACAACTTTAGATGATCGTGGGAAACCTT 1543	Qy	2564	TGGCTCTGGCTAGAGAAAGGATCTGTTGAGGATTTCCTCCVATTTGCAATAATTC 2623
Db	1546	AGTCACAACTTAAATAGTGACGAGATCTGCTGACCTTGGCAAACGATTAAAC 1605	Db	2590	TAGAGTGTGCTAAACGAAAGCTGACTGTTGAGGTTTACATGGAAATGTC 2649
QY	1544	TAGATAAAAGAACACAAATTGGACACGTTGATTAAGTACTGTTAACCT 1603	Qy	2624	CAAATGACATTAAAGGGCAGCTTCAAAACGGAGAGAAATTTGA 2669
Db	1606	TGGATTCCGTGCAAGTTGATTAAGTACTGTTAACCT 1665	Db	2650	AGGATATGATATCATGAAACAGGACCAAAGGCTATGTTG 2695
QY	1604	TCAAGAAGAGGCAAACTTCACTACATGTTGAACTTACAGTGTCTGAAAGT 1663	RESULt 8		
Db	1666	TTCGTAA----CAATAAAACTTGTAGTTAGCTGTTGAGATGTTAAAT 1719	US 09-512-250C-1		
QY	1664	TACCTTACAAACAACTCAAACAACTTCACTACATGTTGAACTTACAGTGTCTGAAAGT 1723	; Sequence 1, Application US/09512250C		
Db	1720	TACAAACAGCAAACTGACTCTTAAATGAGAGTAACTACAGAAATATG 1779	; Patent No. 6518042		
QY	1724	AAAGCTGTGAGAAAGAATGGTAGCTCGTGTAGTTCAAACGCTGCAAGTTCTCCGGGG 1783	; Inventor: Borchert, Torben		
Db	1780	AAGAGGCCAGGATGCCATTGTTAAAGAATATGTCATAATTTCAGCTGTGAGAC 1839	; Inventor: Pedersen (Executor for Lars Christiansen, deceased), Dennis Vind, Jesper		
QY	1784	TGTTGCGATGATGCTGTTGACTGCTGAGTTGCTGAGTTGCTGAGTT 1843	; Title of Invention: A process for Making DNA Libraries In Filamentous Fungal Cells Using Cloned Gene Involved in the Mismatched Repair System		
Db	1840	CAATGCGAGACACTCATGTTGTTAGCTGCTAGTGTGTTGCTCAG 1899	; File Reference: 5718-200-US		
QY	1844	TGGCTGCCACTTGCCAAACTCCPACACAGACCAATTCACTCCACAGGATACAGGAG 1903	; Current Application Number: US/09/512,250C		
Db	1900	TGTCAAATGGACACTGTGTCATATGACGACGCCATTGAGAAAGCAAGGAA 1959	; Number of SEQ ID NOS: 33		
		; Software: Patent in version 3.1			
		; SEQ ID NO 1			
		; LENGTH: 3823			
		; TYPE: DNA			
		; ORGANISM: Aspergillus oryzae			

QY 2407 CATAGAAAATG-----CTGGATACCAATTTCATGTTGACACATT 2454
 Db 3133 AGAACCTGGAAAGTAGTCGCCTCATCGCAGATGTGAGATAG 3192
 QY 2455 GACCCCTTAATCGAAGTAACTATGCTTACCGGTCTTGATGATCAG 2514
 Db 3193 AAGTCAAAGGGAAACCAGTCACCTCTGACCTGGCATTTGACAG 3252
 QY 2515 AGTTGGTATCATGTTGCAATTTCACCGAGTGTGCTGGCT 2574
 Db 3253 TCAATTGGTATCCAAGTTGGCGTAATTGGCTCCGAGAAAGGTGCC 3312
 QY 2575 AGAAAAAGGCACTGAGTGGAGATTCTCC 2609
 Db 3313 GCCCGGAAGGAACTTGAAGACTTACRTC 3347

RESULT 9
 US-09-651-656-2
 ; Sequence 2, Application US/09651656
 ; Patent No. 6340566

; GENERAL INFORMATION:
 ; APPLICANT: MCCUTCHEON-MALONEY, SANDRA
 ; TITLE OF INVENTION: LAWRENCE LIVERMORE NATIONAL LABORATORY
 ; TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE
 ; POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
 ; TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,
 ; FILE REFERENCE: IL-10689
 ; CURRENT APPLICATION NUMBER: US/09/651, 656
 ; CURRENT FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192, 764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 723
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-651-656-2

Query Match Score 7.7%; DB 4; Length 723;
 Best Local Similarity 59.8%; Pred. No. 1.2e-60;
 Matches 446; Conservative 0; Mismatches 270; Indels 30; Gaps 2;

QY 1924 AGGATCCCTGGTGGAAAGTCAGATTGGTTACTCCATCTTAAGCTGAGACTA 1983
 Db 4 AGGATGCTGGTGAAGTCAGATTGGTTACTCCATCTTAAGCTGAGACTA 63
 QY 1984 GTTACGGGAGAGAGTGGTTCAAGATTCATGTTCAAGATTAACATGGCCCTAAACATGGGTGAAGTGGCTTAATCACA 2103
 Db 64 GAAGAAGATAAACAGATGTCACATCATTCCTGCCCATATGGAGTAATCACA 123
 QY 2044 TACATTGGCAAGTGGTCTTCAAGTGGCCCAAGTGGCTGGTCCATGT 2043
 Db 124 TATATTGCAAACTGGGNGTACATGTCACATGCCATATGGAGTAATCACA 183
 QY 2104 GACATGCTACACATTCTATGCTGATGTTTGTGCTGGGGCTGAGATG 2163
 Db 184 GAGTCAGCAAGAGTCCATTGTCGACTGCTTCAATTGAGAGATGCTGAGT 243
 QY 2164 CAGTCAGAGAGTCAATTGAGATGCTGAGCTGATGTTGAA 2223
 Db 244 CAATGCAAAGAGCTTCCACGTCATGGTGAATGTCGAATGCTCCTCG 303
 QY 2224 GGAGCTTGGTTCAGTCAATTGAGTGGCTTCAACTTTATGAGTCAGTGG 2283
 Db 304 TCTGAAACCAAGATTCATGAGTAACTATCATGAGTAAATTAGACCA 363
 QY 2284 GATGGCTACTGATGATGTTGAGTCAGATGTTGAGAATTAAAGACCA 2343
 Db 364 GATGGATTTGGTAGCATGGCTPATATGAGAAAGATGGTGCCTT 423
 QY 2344 ACATGTTGCACTTCACTTCACTGAGTCAGTGGCTGAGTGG 2403

RESULT 10
 US-09-650-855-2
 ; Sequence 2, Application US/09650855
 ; Patent No. 6363355

; GENERAL INFORMATION:
 ; APPLICANT: MCCUTCHEON-MALONEY, SANDRA
 ; TITLE OF INVENTION: LAWRENCE LIVERMORE NATIONAL LABORATORY
 ; CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
 ; TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA
 ; TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA
 ; FILE REFERENCE: IL-10244
 ; CURRENT APPLICATION NUMBER: US/09/650, 855
 ; CURRENT FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/192, 764
 ; PRIOR FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 106
 ; SEQ ID NO: 2
 ; LENGTH: 723
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-650-855-2

Query Match Score 7.7%; DB 4; Length 723;
 Best Local Similarity 59.8%; Pred. No. 1.2e-60;
 Matches 446; Conservative 0; Mismatches 270; Indels 30; Gaps 2;

QY 1984 GTTACGGGAGAGAGTGGTTCAAGATTCATGTTCAAGATTAACATGGCCCTAAACATGGGTGAAGTGGCTTAATCACA 1983
 Db 64 GAGTCAGCAAGAGTCCATTGTCGACTGCTTCAATTGAGAGATGCTGAGT 2103
 QY 2044 TACATTGGCAAGTGGTCTTCAAGTGGCCCAAGTGGCTGGTCCATGT 243
 Db 124 TATATTGCAAACTGGGNGTACATGTCACATGCCATATGGAGTAATCACA 183
 QY 1984 GTTACGGGAGAGAGTGGTTCAAGATTCATGTTCAAGATTAACATGGCCCTAAACATGGGTGAAGTGGCTTAATCACA 1983
 Db 64 GAGTCAGCAAGAGTCCATTGTCGACTGCTTCAATTGAGAGATGCTGAGT 2103
 QY 2044 TACATTGGCAAGTGGTCTTCAAGTGGCCCAAGTGGCTGGTCCATGT 243
 Db 124 TATATTGCAAACTGGGNGTACATGTCACATGCCATATGGAGTAATCACA 183
 QY 2104 GACATGCTACACATTCTATGCTGATGTTTGTGCTGGGGCTGAGATG 2163
 Db 184 GAGTCAGCAAGAGTCCATTGTCGACTGCTTCAATTGAGAGATGCTGAGT 243
 QY 2164 CAGTCAGAGAGTCAATTGAGATGCTGAGCTGATGTTGAA 2223
 Db 244 CAATGCAAAGAGCTTCCACGTCATGGTGAATGTCGAATGCTCCTCG 303
 QY 2224 GGAGCTTGGTTCAGTCAATTGAGTGGCTTCAACTTTATGAGTCAGTGG 2283
 Db 304 TCTGAAACCAAGATTCATGAGTAACTATCATGAGTAAATTAGACCA 363
 QY 2284 GATGGCTACTGATGTTGAGTCAGATGTTGAGAATTAAAGACCA 2343
 Db 364 GATGGATTTGGTAGCATGGCTPATATGAGAAAGATGGTGCCTT 423
 QY 2344 ACATGTTGCACTTCACTTCACTGAGTCAGTGGCTGAGTGG 2403

3 04	TCTGAAACAAAGATCATTAATACTAGTGAATGGAGAGGAACCTTCACCTCAC	3 63
2284	GATGGCTTTGGTTAGCTGGCTATTGTGAGCACATGTGAAAGAATTAAAGCACA	23 43
3 64	GATGGATTGGTTAGCATGGCTATATCGATAACATGCAAAAGATTGCTTT	4 23
2344	ACATTTGTCACACTCTTGTAGCTGACTGATTAGCCACAAAGATGGAGACAT	24 03
4 24	TGGCATTTGCAACCCATTTCATGAACTTACTGCCTGGCAATCAGATACTGT	4 83
2404	GGACATPAGAAAATGTGGATAGCAATTTCATGTTTGCAACATTGACCCTTC	24 63
4 84	AAT-----AATTCATAGTCACAGCATCA-----CCACT	5 13
2464	AATGGGAGCTTAACTATGCTTACAAGGTTCACCAGGTGCTGTGATGAGTTTGT	25 23
514	GRAGGACCTTAACTATGCTTATCAGGTGAAAGAAGSTGTCTGTGATCAAAGTTTGG	5 73
2524	ATTACATGCTGAAATTGCAAAATTTCACCGAGTGTGCTGTGCTAGAAAG	25 83
574	ATTCAATTGCGAGCTTAACTTCCTAAGCTTAAGTGTAAAGTGTCAAACAGIAA	6 33
2584	GCATCGTAGTTGGAGATTCTCTCTTATGCCATATTCCAATGACATTAAAGGGCA	26 43
634	GCCCTGAACTTGAGGAGTTCTGATGATATGGAGATGCCAAGGATATCATGGAA	6 93
2644	GCTTCACAAACGGAAGAGAAGAAATTGCA	26 69
694	CCAGCAGCAAAAGAGTGTCTGG	7 19

SUITE 11
- 08-956-171E-231/c
Sequence 231, Application US /08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: *Staphylococcus aureus* Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/08/956,131
FILING DATE: 26-05-1995

FILING DATE: 20-DECEMBER-1997
CLASSIFICATION: UNKNOWN

PREVIOUS APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark T. Hittman

NAME: MARK C. HUMMEL
REGISTRATION NUMBER: 46-7889

REFERENCE / DOCKET NUMBER : PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439
ELECTION FOR SEC ID NO: 2311

SEQUENCE CHARACTERISTICS:	
LENGTH:	3159 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	double
TOPOLOGY:	linear
SEQUENCE DESCRIPTION: SEQ ID NO: 231:	US-08-956-171E-231
Query Match	4.5% Score 136.8;
Best Local Similarity	51.1%; Pred. No. 8.
Matches	380; Conservative 0; Mismatches
Qy	1640 AAACACGTTAACGGATGGGTTAAAGTTCACTTAT
Db	2300 AACGTTATCCATGTCAGTTTATAACTA
Qy	1700 TCCAGAAGATGTTAGGGACTAACAAAAGCTGT
Db	2240 TTAGGTGCCGAAGCACAAAGCATCGAAATTAA
Qy	1760 AAACACTGCGAGTTTCGAGGTCTCGAGGTGTTGCA
Db	2180 AGGAACTAAAAATAATACTGAACTGTTACAA
Qy	1820 ATGTGTTACTGAGTTTGCCTATTGGCTCC
Db	2120 ATGTGTTACAGATGCTTGCAGAAATTGCTCAA
Qy	1880 ATATCAGTCACACAGATACTGGAGTATTAATA
Db	2066 CATTGTAGGAAATAAAACATTAGA-----A
Qy	1940 AAGCTTAAGATTGGTTAACTCATTCTTAAT
Db	2012 AAAGCTTAATGTTATTAATGCAATGTCCTT
Qy	2000 GCTTCAGGATTACAGGCCAACATGGT
Db	1952 TTATATTTATTACAGGTCCGAAATATGTC
Qy	2060 GTGTGAATGTCCTGATGGCCAAGTGGCTCG
Db	1892 CCATATTAGTATAATGGCCCAATGGACCT
Qy	2120 CTATTCGTGATTGTTGTTGCTCTGTGTC
Db	1832 CTATATTGTCAAATTCACTAGAAATAGGT
Qy	2180 CTACTTTATCAGAAGATGCTGAGCTGCA
Db	1772 GTAGCTTATGTTGAAATGCTAGAGCACAA
Qy	2240 CATTGATTAAATTGATGAGTTGGCCGGGG
Db	1712 GTTGATTATTTCGATGAAATGAGCTGCTG
Qy	2300 CTGGGCTATTGTTGAGCAATGTTGAGAA
Db	1652 CGCAGGCAATGATAGGTGATGAGCAACAA
Qy	2360 ACTTTCATGAGCTGACTGCCATTAG 2383
Db	1592 ATTATCATGAAATGACAACATTAG 1569

RESULT 12 US-08-743-637B-31 Sequence 31, Application US/08743637B
Patent No. 5994066
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OULIFFE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

STREET: QUARLES & BRADY

CITY: MILWAUKEE

STATE: WISCONSIN

COUNTRY: USA

ZIP: 53202-4497

COMPUTER READABLE FORM:

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/143,637B

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/526,840

FILING DATE: 04-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 85-0586-90012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 3754 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: Linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

US-08-637B-31

Query Match Score 135.8; DB 2; Length 3754;
Best Local Similarity 52.6%; Pred. No. 2e-30; Mismatches 302; Indels 12; Gaps 2;
Matches 349; Conservative 0;

Qy 1714 GAGGGATCAAAGCTGCAAGAAATTGGTAGCTGTCAGTCAACAGCTGCAGT 1773
Db 2483 GAGAAGTCAGCAAACCTCGATAACAAATTATGCAATTGAGGTGGCAG 2542
Qy 1774 TTCTCGAGGTGTTGCACTATGCTGGTGAATTGGTAGCTGTCAGTCAACAGCTGCAGT 1833
Db 2543 TACATCCAGGGTACAAGTTCTGCCAAAGGAATTGGTAGCTGTCAGT 2602
Qy 1834 TTGGGGATTGGCTGCCAGTGCCTACACAGACCAATACTACATTCACCA 1893
Db 2603 CTGGGGTCTCTTAATGACTGAGTTAGGGGAGATTCATGGCACTTCAAGT 2653
Qy 1894 GATAAGGAGATAATATACTTGAGGGTAGGATCCTTGTGGAACTCAAGATGG 1953
Db 2654 GATTACAAATGATGATCCGAAAGGG--GCCATGCTGTAAGGTATGGG 2710
Qy 1954 GTTAATCCATCCATGGTGAAGTCGACCTACATTGGCTGGTGTGATGTCCTG 2013
Db 2711 GCTCAGACCTATTCAAATGATTCAAGTGGAGAGATAACGATTCAATGGT 2770
Qy 2014 ACAGGGCCCTAACATGGTGAAGTCGACCTACATTGGCTGGTGTGATGTCCTG 2073
Db 2771 ACAGGGCCAAACATGTTGAGGAACTCATATGCGTCAGTAGCCATGGCGGT 2830
Qy 2074 ATGGCCCAAATGGTGTCCATGGACATGTCACATTGTCATGGTGTGATGTCCTG 2133

RESULT 13
US-08-526-840B-31
Sequence 31, Application US/08526840B
; Patent No. 6001564
GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: QUELLETTE, Marc
; APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIETIC RESISTANCE GENES
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIETIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN . . .
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586-90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
US-08-526-840B-31

Query Match 4.5%; Score 135.8; DB 3; length 3754;
 Best Local Similarity 52.6%; Pred. No. 2e-30;
 Matches 349; Conservative 0; Mismatches 302; Indels 12; Gaps 2;

Qy 1714 GAGGAGTACAAARGCTGTCAAGAAAGATTGTAGCTCGTACTTCAACACGCTGCCGAGT 1773
 Db 2483 GAGAAGTCAGCCACCTCGATAAGAAATATTATGCCATGTGAAGAGTCGGAAG 2542

Qy 1774 TCTCCGGAGGTGTTGCAAGGTATAGCCTGGGTACTTGTGCTTGTTGATGTCTACTGAGT 1833
 Db 2543 TACATCCAGCGTTACAGCTTAGCCAGGATGGCCTGTACAGAGT 2602

Qy 1834 TTGCGGATTGCGTGCAGTCAGTCCACTCCCTACAAAGCCAAATATCGTGTCCACCA 1893
 Db 2603 CTTGGGGTGTGCGTGTG-----AAACCCACATTGTGATCGACATGTTGCTGTGAC 2653

Qy 1894 GATAACAGGAGATATTAPACTTGAGGGTGTAGCACTCTGTGGAAAGGTGAGATTGG 1953
 Db 2654 GATTCAAAATGATATCCGAAAGGG--CGCCATGCTGTTGAAAAGGTTATGGG 2710

Qy 1954 GTTAACCTCCATTCTAAATGACTGTAGACTATGTTAGGGAGAGAGGTTGTTGATATTAC 2013
 Db 2711 GTCAGACCTATATTCAAATGATTCAGATGGAGATAACCAATTAAATGGTT 2770

Qy 2014 AGAGGCCCTAACATGGGGAAAGTCACCTCATGGCAGGTTGCTGTGATGTCCTG 2073
 Db 2771 ATGGGGCAAAATGACTGGGAGCTAACCTATGGTCACTTGGCATGCGGGTT 2830

Qy 2074 ATGGCCCAGTGGCTGTTCCATGTCGAAATGCTACCATTCATGGTGTGATGT 2133
 Db 2831 ATGGCCCAGTGGTTCTATGCTGTCGCCCCATTTACCGATTGTTGATGCG 2890

Qy 2134 ATTTCGCTGTCGTCGGCTGGATGGAGATTCTACTTTATGCAA 2193
 Db 2891 ATTTCGCTGTCGTCGGCTGGATGGAGATTCTACTGAAAGGTTGTTAGGTG 2950

Qy 2194 GAGATGCTTGAGACTGATGTCATGTCGAGCAGATGACTTGGTCAACCTTAAATGCAA 2253
 Db 2951 GGATGATGGAGCCAAATAATGCCATTGGCATGACCAAAACTCTCTCTCTT 3010

Qy 2254 GTGAGTTGGCGGACATCAACTTCACTGGCTGGAGATGGCTTACCTGGCTATTGT 2313
 Db 3011 GTGAAATGGGAGCTGCAACTTATGCGGATGGCTCTGTCAGTCCATC 3070

Qy 3070 GGGCACATGGTGAAGAAATTAAAGCCAAACATGTTGCCAICACTTCACTGAGCTG 2373
 Db 3071 GATATTCATGAGCACATGGCTTAAGACCCACTACATGAGTTG 3130

Qy 2374 ACT 2376
 Db 3131 ACT 3133

RESULT 14
 US-08-961-527-63
 Sequence 63, Application US/08961527
 Patent No. 6,20135
 GENERAL INFORMATION:
 APPLICANT: Charles Kunsch
 TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 391
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII text

Query Match 4.5%; Score 135.8; DB 4; length 7760;
 Best Local Similarity 52.6%; Pred. No. 3.1e-30;
 Matches 349; Conservative 0; Mismatches 302; Indels 12; Gaps 2;

Qy 1714 GAGGAGTACAAARGCTGTCAAGAAAGATTGTAGCTCGTACTTCAACACGCTGCCGAGT 1773
 Db 1802 GAGAAGTCAGCCAACTCGTAACTGAAATATTATGGCATGTTGAAAGGTGCGGAAG 1861

Qy 1774 TTCTCCAGGTTGGGTGGATAGTGTGTTGATCTGATGTTGATGTTACAGTGT 1833
 Db 1862 TACATCCAGCTTGTACAGCTCTAGCCAAAGTGGCCTTGTCTTACAGT 1921

Qy 1834 TTTCGCGATTTGGCTGCACTGGTGCCTAACTCCCTACACAAGGAAATATGTCACACCA 1893
 Db 1922 CTGGCGGTGTGGCTG-----AACCCAGCATTTGATTGACCTGAGTTGGTGA 1972

Qy 1894 GATAACAGGAGATATTATGCTGAAAGGTTGCTGGCTTCTGTTGAGGTCAAAGTTGG 1953
 Db 1973 GATTCAAAATGATTCGGAAAGG-----CGCCATGGCTGTTGAAAGGTTATGGGG 2029

Qy 1954 GTTAACCTCCATTCTGTCATGTCGTCGGCTGGATGGCTTCAGATTTCACATTTC 2013
 Db 2030 GTCAGACCTATATTCACATAGATTCAATAGATTCAATAGATTCAACTGGTT 2089

Qy 2074 ACAGGCCCTAACATGGCTGGATGGAGCTACATTGGGAGGTTGGTCAATGCTG 2073
 Db 2090 ACAGGCCCTAACATGGCTGGAGCTACATGTCATGTCATGTCATGTCATGTC 2149

Qy 2074 ATGGGCCCAAGTGGCTGGTGGCTGAGGAGCTACATTGGGAGGTTGGTCAATGCTG 2133
 Db 2150 ATGGGCCAGCTGGCTCTTGTGAAAGGCCATTATGTCGAAAGGCCATTATGCG 2209

Qy 2134 ATTTCGCTGTCGTCGGCTGGAGATGGCTGAGGAGCTACATTGGGAGGTTGGTCAATGCTG 2193
 Db 2210 ATTTCGCTGTCGTCGGCTGGAGATGGCTGAGGAGCTACATTGGGAGGTTGGTCAATGCTG 2269

Qy 2194 GAGATGCTGAGACTGATGTCGAGTGTAAAGGCTACTGATGATGTTGATGTTG 2253
 Db 2270 GAGATGATGGGGCAATATGCCATTGGCATGGACCAAGACTCTCATCTCTT 2329

Qy 2254 GATGAGTTGGCCGGACATCAACCTTGGCTGGAGATGGCTGAGGAGCTACATTGGCTG 2313
 Db 2330 GATGATGTCAGCTGCACTTGTGCACTTGTGCTGTCATCATC 2389

Qy 2314 GAGCACATGGTGAAGAAATTAAAGCCAAACATGTTGCCACTTCAGAGCTG 2373
 Db 2390 GAATATCCATGAGCACATGGCTGGACCCACTACACCCTCTGACCCATGAC 2449

Qy 2374 ACT 2376
 Db 2450 ACT 2452

RESULT 15
 US-09-543-681A-2786
 / Sequence 2786, Application US/09543681A
 ; Patent No. 05709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709-1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543, 681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO: 2786
 ; LENGTH: 2625
 ; TYPE: DNA
 ; ORGANISM: Proteus mirabilis
 ; US-09-543-681A-2786

Query	Match	Score	Length
Qy	Best Local Similarity 4.4%; Pred. No. 1.3e-29; Matches 284; Conservative 0; Mismatches 252; Indels 0; Gaps 0;	132.8	2625;
Db	1922 GTAGGCATCTCTGTGGAAAGCTCAAGATTGGTAACTCCATTCTTAATGACTCTAGAC 1.981		
Db	1808 GTGGACGTACCCGTGTTGAGAACAGTACTGAGTCACCTTATCTCAAACCTCTAC 1.867		
Qy	1982 TAGTTAGGGAGAGAGTGTTTCAGATTATCACAGGCCCTAACATGGTGAAGGTGCA 2.041		
Db	1868 AACCTGGCCTCAACGGCGTCACTCTTACCGGCCCTAACATGGTGAAGGTGCA 1.927		
Qy	2042 CTCACATTCGGCAGGGTGTGTGATGTCCTGATGGCCCAAGTTGGCTCTGTTCCAT 2.101		
Db	1928 CTCATATGGTCAAGCGCATTAATAGCTACTGGTTATATTGGTAGTTGTGCCCG 1.987		
Qy	2102 GTGACAATGCTACCATTCATCTTCTGTTGATTGATTGTTTGTCTGTTGGCTGGAGATT 2.161		
Db	1988 CAGAAAAACGGTAAATGGCCATATGGCTGGTATTACCCGGTGGCTCTGACG 2.047		
Qy	2162 GCCAGCTGAGGGAGTTCTACATTCTTCTGAAAGATGCTTGACTGCATGCTGTA 2.221		
Db	2048 ATCTGGCTGGCTGGTAACTTATGGGAAATGCAAACTCCAAATATCCCTC 2.107		
Qy	2222 AGGGAGCTAGTATAGATCATGATTAAATGAGTTGGCCTATTGGGACATTGTTGAAGAAATTAAAGCAC 2.281		
Db	2108 ATAATGGCCACTGAAACAGCTTATGGTATGGTAAATGGGAAATGGGCACTTCTACTT 2.167		
Qy	2282 ACCATGGCTTGGTTAGCTTGGCTATTGGGACATTGTTGAAGAAATTAAAGCAC 2.341		
Db	2168 ATGATGGTTTCTCTCGTTGGCTTGGCAAATAATTGGAAATGCAATTAAACCGA 2.227		
Qy	2342 CAACATTGTTGGCACTCACTTCACTGAGCTGACTGCTGATTGGCAACAGATGGGACA 2.401		
Db	2228 TGACACTTGGCCACACATTGGATTAACTGACATGGTAACTGGCAAAACTGAAAGCCA 2.287		
Qy	2402 ATGGACATAGAAAATGTTGGATAGCAATTTCATGTTTGCAACATGAC 2.457		
Db	2288 CTGCCAATATTCACTTATGGCAAGTCACTTGGCAAACTTGGCTTGTGCAAC 2.343		

Search completed: April 9, 2004, 06:53:04
 Job time : 216 secs

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 06:45:13 ; Search time 1017 Seconds
11187.987 Million cell updates/sec
(without alignments)

Title: US-10-029-065-1

Perfect score: 3033

Sequence: 1 ataaaggtaaaaaaaa.....tatctttatgttcaaaaaa 3033

Scoring table: IDENTITY_NUC
Gapext 1.0

Searched: 2475385 seqs, 1875730760 residues

Total number of hits satisfying chosen parameters: 4951170

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Maximum Match 0%

Listing First 45 summaries

Database : Published Applications NA: *

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18: /cgn2_6_ptodata/2/pubpna/us60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	Match Length	DB ID	Description
1	3033	100.0	3033	14	US-10-029-065-1
2	3011.2	99.3	3033	14	US-10-029-065-3
3	1231	40.6	2841	12	US-10-025-114-31788
4	1063.2	35.1	2151	12	US-10-024-539-71262
5	825	27.2	1964	12	US-10-025-114-12669
6	706.4	23.3	1723	12	US-10-025-114-3918
7	685.8	22.6	5307	14	US-10-027-839-48
8	627.6	20.7	1124	12	US-10-024-539-141791
9	422.4	13.9	3080	14	US-10-171-581-78
10	422.4	13.9	3161	15	US-10-062-674-1194
11	420.8	13.9	2805	14	US-10-109-731A-3
12	420.8	13.9	3145	9	US-09-738-657-9
13	420.8	13.9	3145	10	US-09-121-677-9
14	420.8	13.9	3145	10	US-09-160-205-21
15	420.8	13.9	3145	12	US-10-342-887-455

FEATURES

NAME/KEY:	CDS
LOCATION:	(22) .. (2838)
US-10-029-065-1	

RESULT 1

US-10-029-065-1

/ Application US/10029065

/ Publication No. US2003150024A1

/ General Information:

/ Applicant: May, Gregory

/ Applicant: Baszynski, Christopher

/ Applicant: Zhu, Tong

/ Applicant: Kipp, Peter

/ Applicant: Mahajan, Pramod

/ Title of Invention: PLANT MSH2 SEQUENCES AND METHODS OF USE

/ File Reference: 583-9-196213

/ Current Application Number: US-10-029-065

/ Current Filing Date: 2001-12-20

/ Software: PatentIn version 3.0

/ SEQ ID NO 1

/ TYPE: DNA

/ ORGANISM: Nicotiana tabacum

/ NAME/KEY: CDS

/ LOCATION: (22) .. (2838)

Query Match 100.0%; Score 3033; DB 14; Length 3033;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 3033; Conservative 0; Scores 3033; Applier: Qy

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61 CTTAACCTGGATGCTAACGCAAGCTTCTCATCTTCCTGCCTCAAG 120

61 CTTAACCTGGATGCTAACGCAAGCTTCTCATCTTCCTGCCTCAAG 120

Qy 61 GACCCTAGGGCAACTGGCTCTTGTGCGGGACTATATACTCATGGATGAT 180

b	121	GACCTAGGCCAGTGGCCTTTGATCTGTGGAACTATTATACTCATCTGTGAGATGAT	180
y	181	GCAACTTCTATTCGAGAGATAATTACACACAAACAATCGTGTAGCAAGTTCGGTAAT	240
b	181	GCAACTTCTATTCGAGAGATAATTACACACAAACAATCGTGTAGCAAGTTCGGTAAT	240
y	241	AGAGCTGATCCCTTCCACTGTTGAGTAGTGTAGTGTAGAAGAACATAAGTCCTGT	300
b	241	AGAGCTGATCCCTTCCACTGTTGAGTAGTGTAGTGTAGAAGAACATAAGTCCTGT	300
o	301	GACATTCTCTGGAGAGAACTGGGCACTGGTCAAC	360
y	301	GACATTCTCTGGAGAGAACTGGGCACTGGTCAAC	360
b	361	TGGAGACTGTTAAAAGTGAAACCCAGGAATCTGGAGATTGAGATACTGTGTT	420
y	421	GCTAAATAATGAAATGCAAATTCTCGGTAATTGCTCTGGCAACTTCGTCAG	480
b	421	GCTAAATAATGAAATGCAAATTCTCGGTAATTGCTCTGGCAACTTCGTCAG	480
y	481	ANTGATGTAAGTGGCTTGGCTATGTTGAGTAACTAGTAACTAGTAACTAGTAACT	540
b	481	AATGGATGTGAGTGGCTTGGCTTGGCTATGTTGAGTAACTAGTAACTAGTAACT	540
y	541	GAATTCTAGATGATGCACTTCAAAATTGGAGCTCCTTGTGTC	600
b	541	GAATTCTAGATGATGCACTTCAAAATTGGAGCTCCTTGTGTC	600
o	601	AGAGATGTCCTGTACCGGGAGACTGGCAATCCAGGCTATGTTGAT	660
y	601	AGAGATGTCCTGTACCGGGAGACTGGCAATCCAGGCTATGTTGAT	660
b	721	GATTGGTAGGGATCTGGTAGGGCGTCACTGAGAACTCTGGTCACTGAGATTG	780
y	721	GATTGGTAGGGATCTGGTAGGGCGTCACTGAGAACTCTGGTCACTGAGATTG	780
b	781	GTCCTCGGGTCGATCGGGCATCGGGCGTGGGGTGGGGTGGGGTGGGG	840
y	781	GTCCTCGGGTCGATCGGGCATCGGGCGTGGGGTGGGGTGGGGTGGGG	840
b	841	CTTGCCTTGAGGCACTTCAAGAACTTCAACCTCAATGCTTACAGTAC	900
y	841	CTTGCCTTGAGGCACTTCAAGAACTTCAACCTCAATGCTTACAGTAC	900
b	901	ATGAGATTGATTCTGCTGTATGAGAGACTGTAATGTTAGAGCAATCATGCT	960
b	901	ATGAGATTGATTCTGCTGTATGAGAGACTGTAATGTTAGAGCAATCATGCT	960
y	961	AATAAAAATTAGTTAGCTGTTCTGTATGAGAGACTGTAATGCTGAAAT	1020
b	961	AATAAAAATTAGTTAGCTGTTCTGTATGAGAGACTGTAATGCTGAAAT	1020
y	1021	AGGTTATGCACTGTTGAGGCACTTCACTGAGAGACTGTAATGCTGAAAT	1080
b	1021	AGGTTATGCACTGTTGAGGCACTTCACTGAGAGACTGTAATGCTGAAAT	1080
yy	1081	CIGGATTAGTGTCAATCTGTTGAGGCACTTCACTGAGAGACTGTAATGCTGAAAT	1140
b	1081	CIGGATTAGTGTCAATCTGTTGAGGCACTTCACTGAGAGACTGTAATGCTGAAAT	1140
yy	1141	CTGAAAGAATTCTGAGATGATGCTGCGCTGACACAAATCTGAGAGAAAGCCAGT	1200
b	1141	CTGAAAGAATTCTGAGATGATGCTGCGCTGACACAAATCTGAGAGAAAGCCAGT	1200
1201	TTAGNGCAGCTGTGAAACTCTATGAGTCAAGTCAACATGTTGAGATGATGTT	1260	
Db	1201	TTAGNGCAGCTGTGAAACTCTATGAGTCAAGTCAACATGTTGAGATGATGTT	1260
Qy	1261	TTGGAAACGTCATGATGGCAATTGGCAACCTCATGATGGAAACTCTGTT	1320
Db	1261	TTGGAAACGTCATGATGGCAATTGGCAACCTCATGATGGAAACTCTGTT	1320
Qy	1321	GAGAAATGGGTGATGATACTGGATAAGTCAAGCTGCTGTT	1380
Db	1321	GAGAAATGGGTGATGATACTGGATAAGTCAAGCTGCTGTT	1380
Qy	1381	GACCTTGATCAACTTGAGATGGGAGATACTGATGTTGCAATGACCCAAATTAA	1440
Db	1381	GACCTTGATCAACTTGAGATGGGAGATACTGATGTTGCAATGACCCAAATTAA	1440
Qy	1441	TCTGCTCTGAGGGATGCAAGAGACATGGGCAAAATTCAATTGCAAAACAA	1500
Db	1441	TCTGCTCTGAGGGATGCAAGAGACATGGGCAAAATTCAATTGCAAAACAA	1500
Qy	1501	ACTGCGAAATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT	1620
Db	1501	ACTGCGAAATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT	1620
Qy	1561	TTTGGGACACTCTCTGAGATTCCAATGAACTGAGATGGGAGCTGAAAT	1680
Db	1561	TTTGGGACACTCTCTGAGATTCCAATGAACTGAGATGGGAGCTGAAAT	1680
Qy	1621	TCTCACTACATTGTTCTGAAACAGGTGATTGATGGGTAAAGTTCACCTATACAAAAACTC	1740
Db	1621	TCTCACTACATTGTTCTGAAACAGGTGATTGATGGGTAAAGTTCACCTATACAAAAACTC	1740
Qy	1681	AAAAGACTAGGATGATGTTGAGATGTTGAGATGTTGAGATGAAAGCTGTCAGAGAA	1740
Db	1681	AAAAGACTAGGATGATGTTGAGATGTTGAGATGTTGAGATGAAAGCTGTCAGAGAA	1740
Qy	1741	TTGGTAGCTCTGTAGTTGAGTCAAACGCTGGAGTTCTCCAGGTTGTCAGGTATAGCT	1800
Db	1741	TTGGTAGCTCTGTAGTTGAGTCAAACGCTGGAGTTCTCCAGGTTGTCAGGTATAGCT	1800
Qy	1801	GGTGTGACTCTGCTGAGTTGCTGAGATGTTGCTGCACTGTCAGTGGCCC	1860
Db	1801	GGTGTGACTCTGCTGAGTTGCTGAGATGTTGCTGCACTGTCAGTGGCCC	1860
Qy	1861	ACTCCCTACAAGGCAAAATATCGTCCACAGATACTGGGATTTACTTGAGGG	1920
Db	1861	ACTCCCTACAAGGCAAAATATCGTCCACAGATACTGGGATTTACTTGAGGG	1920
Qy	1921	TGTAGCCATCTCTGCTGAGCTGAGATGGTTAACTCCCTAATGACTGTGAA	1980
Db	1921	TGTAGCCATCTCTGCTGAGCTGAGATGGTTAACTCCCTAATGACTGTGAA	1980
Qy	1981	CTAGTTAGGGAGAGGTTGCTGATGTTCACTGGCCCTAACTGGGTGGAAAGTCTG	2040
Db	1981	CTAGTTAGGGAGAGGTTGCTGATGTTCACTGGCCCTAACTGGGTGGAAAGTCTG	2040
Qy	2041	ACCTACATTCTGGCACTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG	2100
Db	2041	ACCTACATTCTGGCACTTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG	2100
Qy	2101	TGTGACAATGCTGACATTCTGATGTTGCTGATGTTGCTGATGTTGCTGATG	2160
Db	2101	TGTGACAATGCTGACATTCTGATGTTGCTGATGTTGCTGATGTTGCTGATG	2160
Qy	2161	TGCCACCTGAGGGACTTCTACTTTGATGCTGAGCTGCTGAGCTGCTGAGAT	2220
Db	2161	TGCCACCTGAGGGACTTCTACTTTGATGCTGAGCTGCTGAGCTGCTGAGAT	2220
Qy	2221	AAAGGGACTCTGATGAGATCATTTGATGTTGAGTCACTGGGACATTAAC	2280
Db	2221	AAAGGGACTCTGATGAGATCATTTGATGTTGAGTCACTGGGACATTAAC	2280
Qy	2281	TACGAGGGCTGTTGGTTAGCTGGGCTTACTTGTGAGCACATTGTTGAGAAATTAAAGCA	2340
Db	2281	TACGAGGGCTGTTGGTTAGCTGGGCTTACTTGTGAGCACATTGTTGAGAAATTAAAGCA	2340

Dy	2341	CCACATGTTGCCACTACTTCTAGACTGAGCTGATTAGCCACAGAACGGAC	2400
Db	2341	CCACATGTTGCCACTACTTCTAGACTGAGCTGATTAGCCACAGAACGGAC	2400
Dy	2401	AATGGACATAAGAAAATGTGGATAAGAAATTTCATTTTGACACATTGACCT	2460
Db	2401	AATGGACATAAGAAAATGTGGATAAGAAATTTCATTTTGACACATTGACCT	2460
Dy	2461	TCTAATGCCAAGCTTAATGCTTCAAGGTTCACCGAGTCTGGCTCTGGAGAA	2520
Db	2461	TCTAATGCCAAGCTTAATGCTTCAAGGTTCACCGAGTCTGGCTCTGGAGAA	2520
Dy	2521	GCTATTCTATGTTGCCAATTTCCTCCAGGAGTCTGGCTCTGGCTCTGGAGAA	2580
Db	2521	GCTATTCTATGTTGCCAATTTCCTCCAGGAGTCTGGCTCTGGCTCTGGAGAA	2580
Qy	2581	AGGCATCTCAGTTGAGGATTCTCTCTCTATTGCCAATTCCATGCAATTAAAGAG	2640
Db	2581	AGGCATCTCAGTTGAGGATTCTCTCTCTATTGCCAATTCCATGCAATTAAAGAG	2640
Qy	2641	GCACTTCAAACGGAGAGAAATTGACGCCATTGAGCTGTTAGGTACTGCCAGA	2700
Db	2641	GCACTTCAAACGGAGAGAAATTGACGCCATTGAGCTGTTAGGTACTGCCAGA	2700
Qy	2701	GCTCGGCAATTCTTCAAGGATTCTCGCTCACTGGATAAGATGGATCCAAAGCTG	2760
Db	2701	GCTCGGCAATTCTTCAAGGATTCTCGCTCACTGGATAAGATGGATCCAAAGCTG	2760
Qy	2761	GTCAGGCAAAAGTGGCAAAATGAAACCGACCTGAGGGATCAGTCTGACTCTCAC	2820
Db	2761	GTCAGGCAAAAGTGGCAAAATGAAACCGACCTGAGGGATCAGTCTGACTCTCAC	2820
Qy	2821	TGGCTTCAGAATTCTTAAATTCTTCAGTTAGAACATCTCTGTGAGCTTG	2880
Db	2821	TGGCTTCAGAATTCTTAAATTCTTCAGTTAGAACATCTCTGTGAGCTTG	2880
Qy	2881	GGGGGGATGATACTTATGGGTTTGTGGATAATAACTTAGCCATTCTGTAACCTTCATT	2940
Db	2881	GGGGGGATGATACTTATGGGTTTGTGGATAATAACTTAGCCATTCTGTAACCTTCATT	2940
Qy	2941	TAATCTTACCCCCAACATGATCTCTGAACTTCTGAGCTGTTTGTGATCTGTTG	3000
Db	2941	TAATCTTACCCCCAACATGATCTCTGAGCTGTTTGTGATCTGTTG	3000
Qy	3001	TAATGTAAGCTTATCTGTAATCTGTCAGTAAAGAAAAA	3033
Db	3001	TAATGTAAGCTTATCTGTCAGTAAAGAAAAA	3033

RESULT 2

QY	670	AGATCGCCGCTGATGGTACTGAAGAAACACTGAATTAAAGGGAGAGTTGGTA	729
Db	670	AGATCGCCGCTGATGGTACTGAAGAAACACTGAATTAAAGGGAGAGTTGGTA	729
QY	730	CAGGATCTGGTAGGCCTCAAGGGTTCAGTAGAACCTCTGGTCAGAATTGGTCTCTGGG	789
Db	730	CAGGATCTGGTAGGCCTCAAGGGTTCAGTAGAACCTCTGGTCAGAATTGGTCTCTGGG	789
QY	790	TTCGAATGPGCATAGGCCGTTGGCGGATACCTTCTTGTGAGAACTACTTGCGGAT	849
Db	790	TTCGAATGPGCATAGGCCGTTGGCGGATACCTTCTTGTGAGAACTACTTGCGGAT	849
QY	850	GAGGCAACTATGGAACTATAAGCTCAAAACAATTACAGCTCAATAGTTACATGAGATTA	909
Db	850	GAGGCAACTATGGAACTATAAGCTCAAAACAATTACAGCTCAATAGTTACATGAGATTA	909
QY	910	GATTCCTGCTATGAGGACTGAAATGTTATGGAGGAAATAGATGCTAAATAAAT	969
Db	910	GATTCCTGCTATGAGGACTGAAATGTTATGGAGGAAATAGATGCTAAATAAAT	969
QY	970	TTTAGCTTGTGCTGATGATGAACTGCTGAAATGGTAAAGGTATTCG	1029
Db	970	TTTAGCTTGTGCTGATGATGAACTGCTGAAATGGTAAAGGTATTCG	1029

QY	1030	CACATGTGGCTGAAGCRAACTTTACTAGATGTAAGAAGAGATTAACTGTAGGGCTGGATTATA	1089	2110.0	GCTTACCATTTCTATTCCUGATTTGTTGCTGTTATTTCGCTGTTGGCCTGAGAGATTGCCAGGCTG	2169
Db	1030	CACATGGGTGAGCAACCTTACTAGATGTAAGAAGAGATTAACTGTAGGGCTGGATTATA	1089	2110	GCTTACCATTTCTATTCCUGATTTGCTGTTATTTCGCTGTTGGCCTGAGAGATTGCCAGGCTG	2169
QY	1090	GTTCAATCATTCTGGAGGATGCTGGCCTTGCCAAAGATTGAGCTTGAGATCTGAAAGAA	1149	2170	AGAGGAGTTCTCCTACTTATGCGAGAGATGCTGTTGAGACTGCATGTTGAAAGGACT	2229
Db	1090	GTTCAATCATTCTGGAGGATGCTGGCCTTGCCAAAGATTGAGCTTGAGATCTGAAAGAA	1149	2170	AGAGGAGTTCTCCTACTTATGCGAGAGATGCTGTTGAGACTGCATGTTGAAAGGACT	2229
QY	1150	ATTTCAGATTTGAGCTGGCTGACACATCTTGAGGAAAGAGCCGTTAGTGAC	1209	2210	ACTGATAGATCATTGATAATTGAGCTTGAGATCTGAAAGATTGAGCTTGAGCTGAACTTG	2289
Db	1150	ATTTCAGATTTGAGCTGGCTGACACATCTTGAGGAAAGAGCCGTTAGTGAC	1209	2230	ACTGATAGATCATTGATAATTGAGCTTGAGATCTGAAAGATTGAGCTTGAGCTGAACTTG	2289
QY	1210	GTTGAAAACCTCTATCGTCAAGTACCAAGTAGTACCATATAAACAGTTGGAGACT	1269	2290	TTCGGTTAGCTGGCTTATTGAGAGATCTGTTGAGAAATTAGGACCAACATG	2349
Db	1210	GTTGAAAACCTCTATCGTCAAGTACCAAGTAGTACCATATAAACAGTTGGAGACT	1269	2290	TTCGGTTAGCTGGCTTATTGAGAGATCTGAAAGATTGAGAAATTAGGACCAACATG	2349
QY	1270	CATGATGGCAATTGCAACATCTCATCGGAAAGGTATTGATTCTCTAGAGAAATGG	1329	2350	TTCGCCACTCTCCTACTTCTAGTGGCTGACTGCTATTAGCCACAAAGATGGTAA	2409
Db	1270	CATGATGGCAATTGCAACATCTCATCGGAAAGGTATTGATTCTCTAGAGAAATGG	1329	2350	TTCGCCACTCTCCTACTTCTAGTGGCTGACTGCTATTAGCCACAAAGATGGTAA	2409
QY	1330	ACTGATGATACTGATACTGATGTAAGTACCAAGTACCATATAAACAGTTGGAGACT	1389	2410	AAGAAAATGCTGGGATGCAAAATTTCATGTTTGACACATTGACCTCTTAATGTC	2469
Db	1330	ACTGATGATACTGATACTGATGTAAGTACCAAGTACCATATAAACAGTTGGAGACT	1389	2410	AAGAAAATGCTGGGATGCAAAATTTCATGTTTGACACATTGACCTCTTAATGTC	2469
QY	1390	CAACTTGAGATGGAAATACTGATGTTCTCTGCAATACTGCTCTG	1449	2470	AACGTAATATGCTTAACTGGTTTACAGGGTCAACCGGGCTTGCTGATGAGTTTG	2529
Db	1390	CAACTTGAGATGGAAATACTGATGTTCTCTGCAATACTGCTCTG	1449	2470	AACGTAATATGCTTAACTGGTTTACAGGGTCAACCGGGCTTGCTGATGAGTTTG	2529
QY	1450	AGGATGAGCAAGAGACATTGAGGGACAAATTCATAATTGCAAAACAACTGCCAT	1509	2530	GTGCTGAATTGGAAATTTCACCGGTTCTAGGGTACTGCCAGACTGCTTC	2589
Db	1450	AGGATGAGCAAGAGACATTGAGGGACAAATTCATAATTGCAAAACAACTGCCAT	1509	2530	GTGCTGAATTGGCAATTTCACCGGCTTCAGGGTACTGCCAGACTGCTTC	2589
QY	1510	GATCCTGATCTACCTTGTAACTGATGAAACACATTGGAC	1569	2590	GAGTGGAGGATTCTCCTATTGCCATAATTGACATAAGGGAGCTCTCA	2649
Db	1510	GATCCTGATCTACCTTGTAACTGATGAAACACATTGGAC	1569	2590	GAGTGGAGGATTCTCCTATTGCCATAATTGACATAAGGGAGCTCTCA	2649
QY	1570	GTCCTGAGAACTACCAAGAAGAACCAAACGAGCTAAATCTCACTAC	1629	2650	AAAGGAAAGAGAAATTGACCTGCCATGAGCTGCTACTGCCAGCTGGCAA	2709
Db	1570	GTCCTGAGAACTACCAAGAAGAACCAAACGAGCTAAATCTCACTAC	1629	2650	AAACGGAAAGAGAAATTGACCTGCCATGAGCTGCTACTGCCAGCTGGCAA	2709
QY	1630	ATTGTCCTCGAAACAGCTGATGGGTTAAGTTCACTTCAAAACTA	1689	2710	TTCTTACAGGATTTCGCTGCTGATGTTGAGCTTAACTTCGCTGAA	2769
Db	1630	ATTGTCCTCGAAACAGCTGATGGGTTAAGTTCACTTCAAAACTA	1689	2710	TTCTTACAGGATTTCGCTGCTGATGTTGAGCTTAACTTCGCTGAA	2769
QY	1690	GAGATCTGAGTTTCAAGAGTTGAGGACTACAAAGTCGAGCTAAATTCTC	1749	2770	AACTTCTTTAACTCTCACTGTTGAGAACTATCTCTGTAAGGCTTGA	2829
Db	1690	GAGATCTGAGTTTCAAGAGTTGAGGACTACAAAGTCGAGCTAAATTCTC	1749	2770	AACTTCTTTAACTCTCACTGTTGAGAACTATCTCTGTAAGGCTTGA	2829
QY	1750	CGTGTAGTTAAACAGCTGGGAGTTCTGGAGTTGAGCTTGTGTTACT	1809	2830	CAATTCTTTAACTCTCACTGTTGAGAACTATCTCTGTAAGGCTTGA	2889
Db	1750	CGTGTAGTTAAACAGCTGGGAGTTCTGGAGTTGAGCTTGTGTTACT	1809	2830	CAATTCTTTAACTCTCACTGTTGAGAACTATCTCTGTAAGGCTTGA	2889
QY	1810	GCTGAGTTGGATGTTGTTACTGAGTTGGGATTGGCTCAGTTGCCAACTCC	1869	2890	GATACTTATGCTTCTGTTGAGGTTCTGTTGAGGTTCTGTTGAGG	2949
Db	1810	GCTGAGTTGGATGTTGTTACTGAGTTGGGATTGGCTCAGTTGCCAACTCC	1869	2890	GATACTTATGCTTCTGTTGAGGTTCTGTTGAGGTTCTGTTGAGG	2949
QY	1870	ACAAGACCAAATACTGTCACCAAGATACTGAAAGGTAGGCT	1929	2950	ACCCAAACATGATCTCTGTAATCAGGGACTTTGTATGCTTCTGTTA	3009
Db	1870	ACAAGACCAAATACTGTCACCAAGATACTGAAAGGTAGGCT	1929	2950	ACCCAAACATGATCTCTGTAATCAGGGACTTTGTATGCTTCTGTTA	3009
QY	1930	CTTGTGTGGAGGCTAGATGGTTAACTCCATTCTTAATGACTGTCAC	1989	3010	GCGTTATCTTATGGTCAAAAA	3033
Db	1930	CTTGTGTGGAGGCTAGATGGTTAACTCCATTCTTAATGACTGTCAC	1989	3010	GCGTTATCTTATGGTCAAAAA	3033
QY	1990	GGAGAGAGTTGGTTGATGCTGTTGAGTTACATGGCCCTAACATGGT	2049			
Db	1990	GGAGAGAGTTGGTTGATGCTGTTGAGTTACATGGCCCTAACATGGT	2049			
QY	2050	GGGCAGGGTTGGCTGATGCTGTTGAGTTGCTGTTGAGGTTGACAA	2109			
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RESULT 3
 US-10-425-114-31788
 Sequence 31788, Application US/10425114
 Publication No. US2004004888A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jie,dong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovacic, David K.

APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO: 31788
; LENGTH: 2841
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73219B02_FLI
US-10-425-114-31788

Query Match 40 6%; Score 1231; DB 12; Length 2841;
Best Local Similarity 68.0%; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 820; Indels 9; Gaps 3;

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Db 1 TGCCAGCGTGTGCAAGGCTATGGCTATGGCTTCACATTTGGTGAAGGAC 50

Qy 321 GGACCGTACTCTGAACTATGAGCTGAACTCTGAGACTGGTCAAATCTGAGACTGGTAAAGTGG 380
Db 61 TGAOTCTACATTGGAACTCTATGGGAAGTGGTAAATGGAAATCCAAAGTCCGG 120

Qy 381 AACCCCCAGGGAAATCTGGAAATTGGGATATTCTGTTGCTAAATAATGAAATGCAA 440
Db 121 AACACCTGGAAATATTGGTAACTTGGACATTCGGTCAAAACAATCGAAGA 180

Qy 441 TTCTCGGTGATTCGCTCTGGCTCCAAACTTCGGCTCAGATGGATGCGAAGTTGGCT 500
Db 181 TTACACCGTGTGCTTGGCTTCCAGGCTGCCGGAAAGTCAGCTGTATGGGCT 240

Qy 501 AGGPDATGTTGAAATTACTAGAGACTCCTGTTAACGAAATTCTAGATGATGCC 560
Db 241 TAGTTTTGGATATGACCHATAGGAAGCTTGGTGGCTGATTCGGAGATAGCCG 300

Qy 561 CTTCACAAATTGGAGCTGCTTGGCTTGGCTCTGGTTGAGAAATGTCCTGTACCAAGC 620
Db 301 ATTCACTAATGTTGATCAGTCCTTGTCAATAGTGGCAGGACTGCTTCGCCGC 360

Qy 621 GGAGACTGGAAATCCAGTGTATACAGGCCATATGGCTGAGCAATATCTGAGTGGCGT 680
Db 361 AGATTCGTGAAATCATCCATGCTAAACCCCTTCAGACCTCAATAGTAATGT 420

Qy 681 GATGGTAACTGAAAGAAAGAACTGAATTTAAAGGGAGATTTGGTACGGATCTGG 740
Db 421 TCTGTGTAAGCTGAAAGGGTCACTGAGATCTGGTCAAGATCTGG 480

Qy 741 TAGGTGCTGTAAGGGTCACTGAAACCTGTTGAGATTGCTCTGGCTGAGATGTGC 800
Db 481 TAGAAATAATCAGGTTCTGGTCACTATCTCAGTGTCACTATCTCAGTTGACTATGC 540

Qy 801 ATCAGSGCCTTGGGGTGCATACCTCTTATGCGAACTACTGGGATGAGCAACTA 860
Db 541 TCTTGGTCCCCTTGGAGCTCTTATGCTGAGCTTGGCTGAGATGACTA 600

Qy 861 TGGAAACTACAGTCAAACATAACACCTCAATAGTAACTGAGATTGATGTC 920
Db 601 TCGAAATTACAACTAGAAGTACATTGAACTTACAGTAACTGAGATTGATGTC 660

Qy 921 TAGTAGAGCACTGAATGAACTGTTGAGACCAATCTAGATGCTGATAAAATTAGCTTGT 980
Db 661 ACTTCGAGCATTAACATTCGAGAAAGGAAACTGATGTAACAGAACTCACTGTT 720

Qy 981 CGCTCGATGATGAACTGAACTGTTGACTCTGGTAAAGTGTATTGCAACATGTGGCT 1040
Db 721 TCTGTGCTGATGAACTGAACTGTTGACTCTGGTAAAGTGTATTGCAACATGTGGCT 780

Qy 1041 GAAGCAACCCTTACTAGATCTAGAAGAGGTTAACTGTGAGCTGGATTAGTTCATCATTT 1100
Db 781 GAAACACCTCTTAACTGATGTTAATGAAATAACCGACTAGACATGGTCAGCTT 840

Qy 1101 CGTGGAGGATGCTGGCTCTGGCTCAGATTGAGGAGCTCTGAAAGAATTTCAGAT 1160
Db 841 TGTAAGAACCCGAGACTTGTCAAGGATCCTGGGAAACACTTAAAGGATATCGAT 900

Qy 1161 TGAGGGCTGACACRACATCTTGAGGAAAAGGCCAGTTAGTGGCTAAACT 1220
Db 901 TGATGTCTAACATGCTTCCGAAGAAAGTAATCGCTATCTGAGCTTGTGTAAGCT 960

Qy 1221 CTATCGTCAAGTAACGAGTACCCATATTCAGTAAAGTGTGTTGGACAGCTGATGGCCA 1280

Db 961 TTATCGTCTGTTGAGATCCCTACATCAGGCACTTCAGTAAATAATGGCCA 1020

Qy 1281 ATTTCGCAACACTCATCAGGAAAGGTTATTTGATGAGAAATGCACTGATGATAA 1340
Db 1021 ATTTCGAACTTGTGAAAGTTCCTGAAAGTGGCTGAAAGAA 1080

Qy 1341 TCACCTGAAATGAGTCATAGTGTGAAACTCTGTTGAGAACTCTGTTGACCTGAGA 1400
Db 2081 TCGATTGCGGTTCTCTCTGTTCTGTTGAGACGCTATGATCTGCTGAGCTGAGAA 1140

Qy 2401 TGGGATATACTGATGTTCTCTGCAATGACCCAAATTTCAGTGTGAGGGTGGCA 1460
Db 1141 TGGAGATGAACTGAGATATCTCTCTATATCTCTCTGACTTGTGAGTTAGGTGCT 1200

Qy 1461 AGGAGCATGGAGGCAAAATTCAATTTGCAAAACAACTGCACTATGTCATGTTCT 1520
Db 2201 TTCTGTGGTGAAGAACCAATTCAGCTGACGTACAGTGTGATCTGATCTGAT 1260

Qy 1521 ACCPTTGTGATAGCTTAACTGAGTAACTGAGACATTCGACACTCTGAGAT 1580
Db 1261 TTCTGTGAACTGAGCTGAGCTGAGTAAAGGATCCC---TTGCACTGTGTCAGAT 1317

Qy 1581 TACCAAGAAGAAAGCAAAAGTCAGGAGCAGTAAATCTCAGTAACTGTCGAA 1640
Db 3138 GTCAAGAAGAGGAAACAAAGTCAGGAGAAGTCACTTCAGTAACTGCACTTAACTGAA 1377

Qy 1641 AACAGCTGAACTGAGTGGCTTAAAGTICACCTATGAACTCAAACACTGAGATCTGAGT 1700
Db 1378 AACCTGTAAGATGTGTAAGTCAAAATTCTPAAGCTGAAATCTGATCAATA 1437

Qy 1701 CCAGAGAGATGTTAGGGATCACAAAGCTGTCAGAAGATTGTTAGCTGTTGTC 1760
Db 1438 CCAGCCATTCTTGTGATGACATCTGTCAGAAACCTGGTGTGAGTGGT 1497

Qy 1761 AACACTGCGAGTTCTCCAGGGTTGAGGTATAGTGGTGTACTCTGACTTGGAA 1820
Db 1498 GGTTCAGGGACACATCTCAGAETATTGAAATTTGGCAGSTCTGGGAGTTGCA 1557

Qy 1821 TGTGTTACTGATGTTGGCTGAGCTCCCTAACAAAGCCAA 1880
Db 1558 TGTGTTACAAAGTTTGCATTTGCACTGTGCCCAGTTGCTCTATGTTAGCCAGA 1617

Qy 1881 TATCAGTCACCGATACTAGGAGATAATTACTGATGAGGATGTTGAGCTGTC 1940
Db 1618 CTCAGCTGGCTGGATGAAGGAGATACTGTTCTGCTGAGCATCTTGTGCA 1677

Qy 1941 AGCTCAAGATGGTTAACTCCATCCTTCAATGCTGAGCTAGTTGGGAGAGTGTG 2000
Db 1678 GGCAGAGAGGTGTTAACCTTAPACCCATGATTGCACTCTGTGACTCTGGT 1717

Qy 2001 GTTTCAGATATCAAGCCCTAACTGCTGTTGAGCTTACATTGGCAAGGGTGG 2060
Db 1738 GTTTCAGATATCACTGAGACAAATGCGAGGAAATCCATTTAAAGACAGTGG 1797

Qy 2061 TGTGATGTCCTGATGGCCCAAGTGGCTGTTCTGATGTCATGTCATGTCATTC 2120
Db 1798 TGTAATGTTGATGATGAGCAAGTGGTTCTCTTGTGATCAAGCAGGATTAG 1857

Qy 2121 TATCCTGATGTTGATGTTCTCTGTTGGCTGAGATTGCGCTGAGAGGAGTTTC 2180

US-10-424-599-71262	Query Match	Best Local Similaar	Cor
	Matches 1346;		
QY	1069 ATTAA		
Db	1 ATTAA		
QY	1129 TTGAGG		
Db	61 CTGAGG		
QY	1189 AAAAGA		
Db	121 CGACGG		
QY	1249 ATCAA		
Db	181 ATCAA		
QY	1309 ATTGA		
Db	241 CTGGAA		
QY	1369 GAAAC		
Db	301 GAAGC		
QY	1429 GACCC		
Db	361 GACTC		
QY	1489 TTGCAT		
Db	421 TTGCAT		
QY	1549 AAAGA		
Db	481 AACGG		
QY	1669 AACCA		
Db	541 AAGAA		
QY	1669 TATACT		
Db	601 AACAC		
QY	1729 TGTCAT		
Db	661 TGTCAT		
QY	1789 GCAGG		
Db	721 GAATC		
QY	1849 GCCAG		
Db	781 TCTAG		
QY	1909 ATACT		
Db	841 ACTTT		
QY	1969 AATGA		
Db	901 AATGA		
QY	2029 GGTTGG		
Db	961 GTTGG		

2089	TCGTGTTCTCCATGTCAGCATGCTCACATTCTCATTTCTGTTGATGTTGATGTTGCTGTTGTT	2148
1021	TCCCTGTTCCCTGTGACATGCCAGCATATCCTGCATTTGCTGTTGTT	1080
2149	GCGGCTGGAGATGTGCCAGCTGCAACTTCGTGGAGTTTCACTTTATGCAAGAGATGCTTGAACT	2208
1081	GGTGTGTTGACTGTCAACTTCGTGGAGTTTCACTTTATGCAAGAAATGCTTGAACT	1140
2209	GCATCGATCTGTCAGAGGAGCTACTGATAGATCATGGATTATAATTGATGAGTTGGCCGT	2268
1141	GCATCAATTAAAGGAGCTACTGACAGTCCTGATATCATGATGAGTTGGACGT	1200
2269	GGGACATCAACCTACAGATGGCTTGGTTAGCTGGTATTGAGCACATTGTGAA	2328
1201	GGGACATCAACCTATGTGGATTGGCTTGAATGCTGGCCATTGTGAGCATATGTTGAA	1260
2329	GAATTAAAGCAACAAATTGGTTGCACTCACTTCAATGGCTGAACTGCCAAC	2388
1261	GTAATCPAAGCHCCTACTTGTGCAACCACTTCAGAATGCACTGATTGCTT	1320
2389	AAGAATGGAGACAATG--GACATAAGAAAAAATCTGGGATAGCAAATTTCAGTTTT	2445
1321	GAAAATLAAAGCAATGATTCAAGGAACTTGTGGCAACTATCATGTTAGT	1380
2446	GCACACATTGACCCCTTAATCGAAAGTAACTATGTTAACAGGTTACCCGGAGTGTGNG	2505
1381	GCACATATTGACTCATCACTGAAAGGTAACCATGTTAACATGTTGGCTGAGCT	1440
2506	TGTGATCAGAGTTGGATTTCATGTTGCAATTTCACCGAGTGTGNG	2565
1441	TGTGATCAGAGTTGGATTTCATGTTGCGAGTTGCAAAACTCTCTGAAGTGTGTT	1500
2566	GCTCTGGCTAGAAAAGGCACTCGAGTTGGAGATTTCTCTCTGCAATATCCA	2625
1501	ACCTCTAGTTAGAAAAGGCAAGGCAATTAGAAACTTTCTCCCTCTGAAACTCTCTGA	1560
2626	AATGACATTA--AAGAGGAGCTTCAAAACGGAGAGAAATTGACGCCATGACGTG	2682
1561	AATCATACTACAGGGTAGTTCTAACTGAGGCAATTGAAACCGATGACATG	1620
2683	TCTGAGCTACTGCCCAGAGCTCCATTCAGGAAATTTCGTCACATTGCCACTGGAT	2742
1621	TCTCAAGGGGTCGCAAAAGGCTGGCAATTCTAGAACATTGTTGCTCTAGAA	1680
2743	AAGATGGATCCTAACGTTGTCAGGAAAGTTGAGCAAATGAAACCCACCTGGAGAGG	2802
1681	ACCATGACACAAATGCAAGCTTGTGCAAGAGTAAGAACTTACAGATACTTGGAGAG	1740
2803	GATGCACTGTGACTCTCACTGGCTTCAAGGAAATTCTTTAAT	2842
1741	GATGCACTGAAACTCTGTAATTGGTGCACAGTTCTGTAGT	1780

TYPE: DNA	ORGANISM: Zea mays	FEATURE: OTHER INFORMATION: Clone ID: 701162994_FLI IS-10-425-114-12569	Query Match	Score 27.2%	DB 122; Length 1964;
Best Local Similarity	68.8%	Pred. No. 1.e-20;	Score 825;	DB 122;	Length 1964;
Matches 1179;	Conservative	No. Mismatches 525;	Indels 9;	Gaps 3;	
1139 ATCTGAAAGAATTTCGATATTGAGGGCTGACACAAATCTGAGGGAAAGAGGCCA 1198					
1 AACTTAAGGTATCGATATTGATGCTAACATAGTCTCCGAAAGAAATCAGCTGA 60					
61 ATCTGAGCTGTTGAAGCTTATGCTCTGAGAATCCATCAAGGGCA 120					
1199 GTTAGTCACGCTTGAAACTCTATACTAGTCAGTACAGTACCAAGTACCTATATCAAAGTGC 1258					
1259 TTTCGAAACGCTATGATGGCGATTTCGAAACACTCAAGGAAAGGTTATGATCTTC 1318					
121 TCTCTCGCAATTATAATGCCATTTCACATTGATTAAGGTCAAAGTTCTGAAACCGT 180					
1319 TAGAGAAATGGATGATGATGATAATCACCTGAAATAGTCTAGTCAGTCTGGAAACTCTG 1378					
181 TAGAGAAATGGATGCGAAAGATGATTCAGTATGATGTTCTCTCTGAGAGCTTA 240					
1379 TTGACCTTGATCAACTTGAGATGGAAATACATGATTTCTGCAATATGCCAAATT 1438					
241 TTGATCTTGCTGCTGAGCTGAGATGGAGAATCTGAGAATCTGAGTCTCTGACT 300					
1439 TATCTGCTCTGAGGATGAGCAAGAGCATTCAGGCAAAATTCAATTTCGAAAC 1498					
301 TGGGTGTAFACTAAGGGTAGCTTCTGGTTGAAACCACATAAACATCTGACCTCG 360					
1499 AAACCTCCAATGATCTGATCTACCTATTGATAAAGTCACCTAAACTCTGAAACAC 1558					
361 ATACAGCTTGTGATCTGATCTGATCTGATCTGATAAAGCTGAAACTGAAAGTCCC 420					
1559 AATTGGACAGTCCTCTGAAATTACCAAGAAAGAACCAAAAGTCAGGAGCTAA 1618					
421 --TTGGACATCTGTCGAAATGTCGAATGTCGAATGTCGAATGTCGAATCTCA 477					
1619 ATTCTCACTATGGTCTGCTGAAACAGCTAACGATGGGGTAAGTTACCTATACAAAC 1678					
478 CTGGCGGCTACTTAACTATGAACTCTGTAAGATGGTGTAAAGTTCACAAATCTAACG 537					
1679 TCAAAAACCTACAGGAGTCAGTCTCAGGAGATCTGAGGAGTACAACAAAGCTGCAAG 1738					
538 TGAAALATCTTATGTGATCAATGACCGCATGTTGGTGTGAACTGTTGAAAAA 597					
1739 AATTGGTAGCTGCTGTAACACCTGCGAGTTCTCCGGGGTTGCGAGTTAG 1798					
598 AGGTGTTGTTGCTGATGTTGAGGGTTTACGGCACATTCTCAGGGTAAATTCTG 657					
1799 CTGGTGTACTCTGCTGAGTTGATGTTACTGAGTTGCGGATTTGCTGAGTTGCC 1858					
658 CTGCASTTCTGCTGGGGTTGGATTTACAAAGTTTGCTGATTTGCAACTAGTGTGCC 717					
1859 CAACTCCCTACAAAGACCAAAATCTGTCACCGAGTACAAGGAGATTAACTCTGAA 1918					
718 CAGTTCTTATGCTTACGCCAACATCTGCTGGTTCAAGTAACTCTCTAAATGACTG 777					
1919 CGTAGCTGCTCTGCTGAAAGCTTAAGTTGGGTAACTCCATCTCTAAATGACTGTA 1978					
778 GTAGCGAACATCTGCTAGGGCAACAGTGTCTAACTTTATCCCAATGATGTCGA 837					
1979 GACTAGTAGGGAGAGGTTGGTTCAAGTAACTCTGCTGGTTCAAGGAGATACTG 2038					
838 CTCTGTTGAGGGAAAGTGGTTCAAGTAACTGTCAGTCACTGGACAAATGGGAGAA 897					
2039 CGACCTCACTACGGCAGGTTGGTGAATGTCCTGATGCCAACCTGCTGGTTGTT 2098					
898 CCACAAATTATAAGACAGCGTTGGTTGTTGAAATGTTGAGTGTCTCTTGTAC 957					

Qy	1489	TTCGACACAAACTGCOATGATCTGATCACCTATTGATAAGTCACTTAACCTAGAT	1548	186 TTTCATCGAGAGACATATTACACACAACTGGGTATCGACAGTTGGPAAATAGGCC	245
Db	963	CTGCACCTGGATACAGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAA	1022	1156 TTTCATCGAGAGACATATTACACACAACTGGGTATCGACAGTTGGPAAATAGGCC	1215
Qy	1549	AAGGAAACCAATTGGACACCTCTCAGAATTTACCAAGAAAGAACCAAGTCAAGCTGG	1608	246 TGAATGCCCTTCAGTTAGTGTGAGTAGAAACATTTGAAACAAATAGCTGTGACAT	305
Db	1023	AAGGATCC---TTGGCATGTTGTCAGAATGTCAGAACAGAACAGAACAGTCAAG	1079	1216 AAATGCTCTTCAGCTAGTAAAGTAACTAGGAACTAGTCAAGCTGAAAGTGTGAT	1275
Qy	1609	AACCGAGCTAAATCTCACTACATTGTTCTGAACTGAACTGAACTGAACTGAACTG	1668	306 TCTCTTGAGAGAATGCAACCCPACTCTGAACTATATAGGGCAAGTCTCAAACCTGGAG	365
Db	1050	AAGAACATCAGTCAGCTGAGCTACTAATCATGAAACTCTAACATGTTACA	1139	1276 TCCTCTTGAGAGAATGCAACCCPACTCTGAACTATATAGGGCAAGTCTCAAACCTGGAG	1335
Qy	1669	TATACAAAACCTAAAAACTGAACTTCAAGAGATAGTTCAGAGATGTAGGGGACAAAGC	1728	366 ACTCGTAAAAAATGGAAACCCAGGGAACTCTGGAACTTTGAGGATAATTCTGTTGCTAA	425
Db	1140	AATTCTAACGTGAAAAATCTCACTGATAATACAGGATTGTTGGTAGTACAGT	1199	1336 ACTCGTAAAAAATGGAAACCCAGGGAACTCTGGAAACCTGGTAACTTGGCTGAA	1395
Qy	1729	TGTCAGAAAGAATTGGTAGCTGTGACTTCAACAGTGCAAGTTCCAGGTTCTT	1788	426 TAATGAAATGCAAAATTCTCCCGTGTATTGCTGCTCTGCTCCAAACTCTGGTCAAGATGG	485
Db	1200	GTTCAGAAAAGGTGGTTGGTAGTACTGAGCTGAGGTTTCAAGGTTCAAGGTTATT	1259	1396 CAATGAAATGCGGGACACACCAGTTGTCCTCCAACTTCAAGTTTCAGATGGCAG	1455
Qy	1789	GGAGGTATAGCCAACTCCCTACACAGACCAAAATCTGTCACAGAGATACTGGAGATT	1848	486 ATCTGAACTTGGGTTAGCTGAACTATGTTGACCTAGCTGGAGAGTCTGAGCTGAGT	545
Db	1260	GAAATTTGGCGAGTCTGTGGAGTTGGTAGTACTGAGCTGAGTTCAGTGGCA	1319	1456 TCCTGAACTTGGGTTAGCTGAACTATGTTGACCTAGCTGGAGAGTCTGAGT	1515
Qy	1849	GCGAGTGGCCAACTCCCTACACAGACCAAAATCTGTCACAGAGATACTGGAGATT	1908	546 TCTAGATGATGCCACTTCAAAATTGCACTTGTGCTGCTGCTGCTGCTGAGA	605
Db	1320	ACTAGTTCCTCCAACTTCCCTATGTTAGGCCAGACATCTGCTCGGTATGAAAGGATTT	1379	1516 TCCTGATGATGCCACTTGTGCTGCTGCTGCTGCTGCTGAGTCAAGGCAAAAGA	1575
Qy	1909	AATCTGAGGGGTGGCATCCTGTTGAGGCTCAAGATGGGTAACTCCATCTT	1968	606 ATGCTCTGTTACCGCGGAACTCTGGCAATCCGCTTATGTTGCTATGTTGAA	665
Db	1360	GTTCTACTGGTAGCAGACATCTGCTAGGGCAZAGATGGTAACTTACCTTACCC	1439	1576 ATGCAATTTCAGCGTAACTCCGCAAACTCCGCAATCCGCAATCTGAACTTCTC	1635
Qy	1959	AATGACTCTGAGTCACTAGTAACTGGAGAAGTGTGTTGATTCAGGGCTAAACATG	2028	666 ATCTAGATGCGCTGTTGAGTAACTGAAAGAAGAAACTCTGATTAAGGGAGAGTT	725
Db	1440	AATGATTCGACTCTGGTAGGCAAGGAAAGTGTGTTGATCATCTGGACAAACATG	1499	1636 GGAGAGGTGTGGCTGTTGATACAGGGAGAAACAGGAGTTAAAGAAGAGTT	1695
Qy	2029	GCTGGAAAGTGCACCTACATGGCAGGTTGG	2060	726 GGTACAGGATCTGGTAGGCTGTCAGGGTTCAAGGGTCACTGGAACTCTGGCTC	785
Db	1500	GAGGAARATCCACATTATAAGACAGTTAG	1531	1696 ACATTCAAGATCTAAAGATTTGGGGATAATGAGCTGTTAGAGATTGGTATC	1755
Qy				786 TGGGTTGGAAATGGCATAGGGCTTCTGGGTGCACTTCTTCTGGGAACTACTTGC	845
Db				1756 CGGGTTGGACCTTGGGAACTCTGGCTCTGGCTCTGGCTCATCTGGCTCTC	1815
Qy				846 GATGTGAGGAACTATGGAAACTATGAAACTTCAAACTACAACTTCAATAGTTACATGAG	905
Db				1816 AAATGAGGATAACTATGGAAACTTCAAACTGGCATATGTTGAGTCTGAGT	1875
Qy				906 ATTAGATTCTGCTGCTGATGAGGACTGAACTTCAAGATGCTAAATAAA	965
Db				1876 ACTTGACTCTGAGCTGAGCTGAGGGCTGTAATGTGAGGAAACACTGCTAA	1935
Qy				966 AAATTGAGCTGTTGGCTGATGAAATAGAACCTGGTAANAGGTT	1025
Db				1936 GATTTGCAATGTTGTTGCTCATGACAGAACATGTAACCTGGTAAGACAT	1995
Qy				1026 ATTGCAATGTTGGCTGAGAACCTTTAGATGAGATACTGGTGA	1085
Db				2056 TATAGTCGATGCTGGCTGAGCAACCCCTCTGGTAAAGGAGATCTGAGCATG	2115
Qy				1146 AGAATTTCAGATATGGCGCTGACACAACTCTGGAGAGAAAAGAGCCAGTTAGT	1205
Db				2116 CGGAATCTCAGATGTTGAGGCTTGGCTCTGGAGAGATGGGGTTACA	2175
Qy				1206 GACGTTGAAACTCTA	1224
Db				2176 GCACATATTAAACTCTAGGTACTTCACTGGCAACTTCATCTCAATGTTAA	2235
Qy				1225 -----	1224

RESULT 7
US-10-270-819-4B
; Sequence 48, Application US/10270839
; GENERAL INFORMATION:
; APPLICANT: Chao, Qimin
; APPLICANT: Grasso, Luigi
; APPLICANT: Suss, Phillip M.
; APPLICANT: Nicolaides, Nicholas C.
; TITLE OF INVENTION: Genetic Hypervariability of Plants for Gene Discovery and Diagnosis
; FILE REFERENCE: AG00021S (MOR-0133)
; CURRENT APPLICATION NUMBER: US/10/270, 839
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328, 750
; PRIOR FILING DATE: 2001-10-12
; SEQ ID NO 4
; LENGTH: 5307
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-270-B39-4B

Query Match Score 685.8; DB 14; Length 5307;
Best Local Similarity 63.4%; Prod. No. 4.e-18; Indels 140; Gaps 1;
Matches 1149; Conservative 0; Mismatches 522;

Qy 126 TAGGCCAGTTGGCTCTTGTATCGTCGGGACTTATCATCTGAGTATGGCAAC 185
Db 1096 TAGGAATTATTGTAATGCAATTGCAAGTATTATACTGGCTATGGTAAATTCAGTCACTGGCATGTTGAAATTCAGT 1155

Db	2236	CAAATTCGATTTCATTGCTCTTATCGAACTCTGAAATTAGTTAGGTATGGT	2295
Qy	1225	-----	- CAGTCAGTACCGAGTACCA 1245
Db	2296	ATTAGTCATTACTAATTAAGCTTCATCTTCTGCAGTCAGCTATAGGT	2355
Qy	1246	TATATGAAAGTGTGGAAGCTGTGATGGCAATTGCAACACTCATGGAAAGG	1305
Db	2356	TTCATGAAACAGCTTGACACAGGAAATTCGATCACTGGAGGAGG	2415
Qy	1306	TATATGATCTCTGAGAATGGNGTATGATANTACCTGAAATTAGTCATGGT	1365
Db	2416	TACCRGAAAGCTTGGCTTATAGATGAGATCACCTGGAAAGTTCATG	2475
Qy	1366	GTGGAACACTCTGTGACCTGTGATCAGTGAATGGAATGAAATGATG	1425
Db	2476	GTTGAGTGTGTTGAGATCTGAGCTTGACGGCTGAAATGGAGATACTG	2535
Qy	1426	TATGACCCAAATTATCTGCTGAGGGTGGAGAGACATTGGAGGCGAACATT	1485
Db	2536	TACGAAACCAATTGGCATCTGTAAGATGAAAGATGAAAGAATGATC	2595
Qy	1486	ATTTCACAAACACTGCCATTGCTGATCACCATTGATAGTCAGTAACTA	1545
Db	2596	GAATTTCACAAAAAGCAGGGATAGACTGTGATCTGAGGGCTCTAAACTT	2655
Qy	1546	GATAAAGAAACAAATTGGACACGTTCTGAAATTACCAAGAAAGAACCA	1605
Db	2656	GACAGCAGGGCAATTGGCATCTGGATCAAGGAAAGGAGCCAGAGTC	2715
Qy	1606	AGGAAGCAGCTAAATTCTCACTACATTGTTCTCGAAACACTTAAGCATGGT	1665
Db	2716	AGGAAGAGTGTGACGMACAGCTTATAGTGTGGAGACTCCAAGCAGT	2775
Qy	1666	ACCTTACAAACTCAAACACTGAGGATCAGTCAGAGATCTGAGGAGTCAAA	1725
Db	2776	ACAAACACAAAGCTAAAAAAGCTGGCGACCAAGTACCAAGTGTGTTAGG	2835
Qy	1726	AGCTGTGAGAAAGAAATTGGTAGCTCTGTAAACAGTGGGTTTCGGAGGTG	1785
Db	2836	AGCTGTGAGAAAGGGCTGGTAGCTCTGTAAACAGTGGGTTTCGGAGGTG	2895
Qy	1786	TTTGCCTGTT 1796	
Db	2896	TGTTAGTTAT 2906	

US-10-424-599-14791	Query Match	Best Local Similar Matches
	Qy 37 GAGGAA	
	Db 92 GACCTA	
	Qy 97 TCATTTC	
	Db 152 TCAATT	
	Qy 157 TATTAT	
	Db 212 TATTAT	
	Qy 217 ACTCGG	
	Db 272 ACAGCT	
	Qy 277 AACATGG	
	Db 332 AACATGG	
	Qy 337 CTATAT	
	Db 392 CTCTCAT	
	Qy 397 GGAGT	
	Db 452 GGCAGT	
	Qy 457 GCTCTT	
	Db 512 GCTTTGG	
	Qy 517 ACTAAG	
	Db 572 ACTAAG	
	Qy 577 TCTGGT	
	Db 632 TCGCAA	
	Qy 637 AGTGTAA	
	Db 692 ACTGAC	
	Qy 696 AAAGAA	
	Db 752 AGAGAA	
	Qy 756 TTCAAGT	
	Db 812 CCCTTAT	
	Qy 816 GTGGCAT	
	Db 872 GGATT	
	Qy 876 CAAACAA	
	Db 932 GCGTAG	
	Qy 936 TGTTAT	
	Db 992 TGTCTT	
	Qy 996 AACCTG	
	Db 1052 GACTTG	

QY	2024	ACATGGCTGAAAGTCCACATTGGCACAGTTGGTGTGAAATGTCCTGATGGGCCAAG	2083	Db	425	ATTGGTATTGGCATATAAGGTTCTCGGATATCCTCTCGTCACTGTTGAGAACATTCTCT	484
Db	2015	ATATGGGGAAATCACAATATTGACAAACTGGTGTGAAATGTCCTGCCCCA	2074	Qy	4119	TTGCTTAATAATGAAATGCAAATTCCTCGGTGATTTGCTCTTGCTCAAACTTCGGTC	478
Qy	2084	TGGCTCGTTGTTCCATGTCACATTCACATTCTATCGTGTATTGTTGCTC	2143	Db	485	TTGGTAACTATGATATGTCAGCTTCATTCGGACTGCATCTTGGCC	544
Db	2075	TGGGGGTTGTTGTCATGGTGTGAGTGTCACTGGACTGCATCTTGGCC	2134	Qy	479	AGATGGATGTGAGTGTGAGTTGCTTAGGCTATGGTGTATACTAAGAGTCCTTGTTAA	538
Qy	2144	GTGTTGGCTGGAGATGGCTGAGAGAGTTCTACCTTTATGCAAGAGATGTTG	2203	Db	545	ATGGCCAGAGACGGTTCGAGTTGGAATTCGATGAAACTAGGACTGT	604
Db	2135	GAGTAGGGCTCATCTCAGTGAAGGAGTCATTGCAACGTTCACTGGTGTAAATGTTG	2194	Qy	519	CAGAATTTCTAGATGATGATGATGAACTTCAGCAATTTCAGTGTAAATCAGGCC	598
Qy	2204	AGACTGATGATGATCTGAAAGGAGTACTGATGATGATTAATTCATGAGTTG	2263	Db	605	GTGAAATTCCTGATAATATCATGTTCCAACTTGTGAGCTCTCATGGAC	664
Db	2195	AAACTGATTCATCTCAGTCTCAGGAAAGGAGTCATTGCAACGAAATGTTG	2254	Qy	599	GCAGAGATGTGTTGACCGGGAGACTGGCAAAUTCCAGTGTAAATCAGGTTG	658
Qy	2264	GGCGTGGGACATCAACCTACGATGGCTTCTGGTTAGCTTCGGCTTATTTGTGAGCACATTG	2323	Db	665	CAAGGGATGTTGTTACCGGGAG--AGAGACTGCTGGAGACATGGGAAACTGAGAC	721
Db	2255	GAAGAGAACTTACGATGGATTGGTTAGATGGCTATPATGAAATACATG	2314	Qy	659	ATGCCAATATCTAGATGGCGCTATGGTAACTGAAAGAGAAACCTGAAATTAAAGGCA	718
Qy	2324	TGAAAGAATTAAGGACCAACATTGTTGCCACTACTTCTATGAGCTGACTGCATTAG	2383	Db	722	AGATAAATCAAAAGGGGAATTCCTGATCACAGAAAGAAAAGGTGACTTTCCACRA	781
Db	2315	GRACAAAGATTTGGCTTTCATGTTGCAACCCATTTCATGAACTTACTGCCCTGG	2374	Qy	719	GAGATTGTTGAGGATTGGTCACTGGATTGGTCTCTGGGTGATGTCATACIT	766
Qy	2384	COACACAGATGGAGCAATGGACATAAGATAAGAAAATGGGATGAAATTTCATGTT	2443	Db	782	AAGACATTTATGGGAACTTCACGGTTGTTGAAGGAAAAAGGGAGGCAATGATA	841
Db	2375	CCAAATCAG-----ATACAAACTGTTTAATATCTACATGTC	2410	Qy	767	CNGTCGAGATTGGTCTCTGGGTGATCAGGGCTTGGGTGATCATTT	826
Qy	2444	TGACACATGACCCCTCTAAATGCAAGCTAACATGCTTACAAGGTTCACCCAGGT	2503	Db	842	GTGCTGTATTGGCAAAATGGGAAATGGGAAATGGGATGTTGCTCATACTGTC	901
Db	2411	CAAGCTCA-----COACTGAGAGACCTTAACATTGCTTATCAGTGAAAGGTG	2464	Qy	827	CMTATGGAGAACTACTTCCGGATGAGCAACATATGAAACTATACACTCAACATACA	886
Db	2375	CCAAATCAG-----ATACAAACTGTTTAATATCTACATGTC	2410	Db	902	AGTTTATGAAACTCTTTATCAGATGATTCACATTGACAGTTGACACTTTG	961
Qy	2564	TGGCTGGATCAGAGTTGGTATTCTGTTGAAATTGGCAAAATTTCCACCGAGTTG	2623	Qy	887	ACCTCATAGTACATGATGAGTATGGGAACTTCTGGTGTGAGTTGTTGAGCA	946
Qy	2504	CTTGTGATCAGAGTTGGTATTCTGTTGAAATTGGCAAAATTTCCACCGAGTTG	2563	Db	962	ACTTCAGCCAGTATAGTAAATGTTGACAGCCCTAACCTGAGCTTACCTTTTCAGG	1021
Db	2465	TCTGTGATCAAACTGTTGGAUTCTGGAUTCTGGAUTCTGGAUTCTGGAUTCTGG	2524	Qy	947	GCATAATGAGTGTAAATAAAAATTAGTGGAGGATGAAATAGAAACCTGACTCTG	1006
Qy	2564	GGCTGGTGGTAGGAAAGGATCTGAGTGGATTCTCCATTGCTTAAATTCC	2623	Db	1022	GTTCCTGTGAAATACTGACTGACTCTAGTCCTGCTGCTGATAAAGTGTAAAA	1081
Db	2525	TAGAGTGTGCTAAACGAAAGGCCTGGAACTTGAGGTTCTAGTATGGAGAATTCG	2584	Qy	1007	CTGGAAATGGTAAAGGTTATGGCAGTGTGAGCAACCTTATAGATGTTGAG	1066
Qy	2624	CAAATGACATTAAGAACGGCAGTTCAAAACGAAAGAGAAATTGAA	2669	Db	1082	CCCTCTAAAGCAAAAGCTTAAACAGTGTAAACAGCTCTCATGGATAAGACA	1141
Db	2585	AGGATATGATCATGAAACAGCACAAAGAACGTTCTGGAA	2630	Qy	1067	ACATTAACTGTTGCTGAGTATGGTCAATCTGGCTGAGTGTGAGCTGCTGAG	1126
Db	10-06-674-1794	Sequence 1794, Application US/10062674		Db	1142	GAATAGGGAGGAGTAAATTAGTGGAGCTTGTGAGAATGTTGAGCTGAGCA	1201
;	;	Publication No. US20040005559A1		Db	1127	ATTGAGCCAGCAT--CTGAAAAGAAATTCAAGATTTGAGGGCTGACACAAATCTTG	1183
;	;	GENERAL INFORMATION:		Db	1202	CTTACAGAAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1303
;	;	APPLICANT: Lorring, Jeonne F.; Kaser, Matthew R.		Qy	1184	AGAGAAAGAGCCAGTTAGTCAGCTTGTAAACCTATCAGTCAAGTACAGTC	1243
;	;	TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS		Db	1262	AAAGACAGCAGCAAACCTACAGATGTTACCGACTCTATCAGGTTACAACTACT	1321
;	;	FILE REFERENCE: PA-0066-1 CIP		Qy	1244	CATATACTCAAATGTTGAGGAAATTCCTGAAATAGTCACTGAAAGTAA	1435
;	;	CURRENT APPLICATION NUMBER: US/10/062,674		Db	1322	CTAATGTTATACGGCTCTGGAAAACATGAGGAAMACACAGAAATTATGTTGGAG	1381
;	;	CURRENT FILING DATE: 2002-01-30		Qy	1304	GCTTATATGATTCCTPAGAGAAATGGGTGATGATAATCCTGAAATAGTCA	1363
;	;	PRIOR APPLICATION NUMBER: US 09/625,102		Db	1382	TTTTGGTGAATCTCTPACTGA-----TCTCCTGGATTCCTGAACTGTT	1483
;	;	PRIOR FILING DATE: 2000-07-24		Qy	1364	TTGTGGAAACTCTGTTGACCTGATTAACCTGAGATGGGAAATACTGATTTC	1423
;	;	NUMBER OF SEQ ID NOS: 2217		Db	1436	TGATGAGAAACACTTAAATGGGATTAATGTTGAAACATTCCTGAAATTC	1495
;	;	SOFTWARE: PERL Program		Qy	1424	CATATGCCCAAAATTATCTGCTTAAGGAGAGCATTGGAGCAAACTTC	1483
;	;	SEQ ID NO: 1794		Qy	139	ACTGGAGACTGTTAAAGGAAACCCAGGGAAATCTGGAGTTGAGGATATCTG	418
;	;	LENGTH: 3161		Qy	138	Query Match Best Local Similarity 51.4%; Pred. No. 3.4e-107; Mismatches 0; Mismatches 1195; Conservative 0; Gaps 7;	418
;	;	OTHER INFORMATION: Incyte ID No. US20040005559A1 251562.5		Qy	137	Query Match Best Local Similarity 13.9%; Score 422.4; DB 15; Length 3161;	418

Db	1496	CATTGATCCTAATCTAGGAAATTAGAAGAATAATGAACTTGGAAAGATGC	1555	Qy	2564	TGGCTCTGGCTAGAAAAGGCATCGAAAGGATTCTGAGTTGGGATTTCCTCTTATGCCATTACATTTC	2623
Qy	1484	ATAATTGCAAAAACCAACTCCCATGATCTGATCTTGTGATCTGAATGCTAAC	1543	Db	2600	TAGATGTRGCTTAAAGAAAGCCCTGGACATCTGGCTTCAAGAGGAACTTGAGGATTCAGTATTTGGAGAAATCGC	2659
Db	1556	GTCACAACTTAATACTGCAACCCAGATCTGGCTTGGACCAACAGATTAAC	1615	Qy	2624	CAATGAAATTAAAGGGAGCTCAAACGGGAAAGAGAAATTTGA	2669
Qy	1544	TAGATAAGAAACAAATTGAGACAGCTPTCAGAAATTACCAAGAAAAG	1603	Db	2660	AGGATATGATATCATGTAACCTGGCAAGAGTGTATCTGGAA	2705
Db	1616	TGGATTCCAGTGCAGTGGATATTACTTCGTTAACCCTGAACTGAAAGATCC	1675				
Qy	1604	TCAGGAGGACGCTAAATTCTCACTACATTGTTCTCGAAACCGTAAAGGATGGCTAAAGT	1663				
Db	1676	TCGTAACATTTAGTACTGATGATATCTAGAAAATGGTTAAAT	1729				
Qy	1664	TACACCTATACAAACTCAAAACCTAGGAAATCAGTTCAGAGATTTGAGGACTACA	1723				
Db	1730	TACAAACAGCAAATTGACTCTTAAATGAGACTATACCAAAATAACAGATAATG	1789				
Qy	1724	AAGGTGTCAGAAAGAATTGGTAGCTCGTGAAGTTAAACGGCTGGGAGTPTCTCGGAGG	1783				
Db	1790	AGAAGGCCAGGATECCATTTAAAGAAATTGTAATATTCTCAGGCTATGAGAAC	1849				
Qy	1784	TGTTTGAGGATAGCTGGTACTCTGCTGGATGTTCTACTGAGTTTGCGGATT	1843				
Db	1850	CAATCGAGAACCTCAATGATGTTGAGCTAGCTGCTGAGCTTGTCTAGCAG	1909				
Qy	1844	TGGCTGCCAGTGTGCCAACCTCCATCACAGAACAAATACTAGTCACCAATACGGG	1903				
Db	1910	TGTCAATGGAGCACCCTGTCATATGTCACCAACGCCATTGTTGAGAAACGACAGGAA	1969				
Qy	1904	ATATTATACTTGAAGGGTAGGCACTCTGTGAAAGCIAAATTTAACTCCA	1963				
Db	1970	GAATTTATTAAGGCAATCCGGATGCTGGCTTGTGAAATGAAATTGCAATTAA	2029				
Db	1964	TTCCTTAATGACTGTAGACTAGTTAGGGAGAGTGGTTCAAGATTATCAGGCCCTA	2023				
Db	2030	TCTCTTAATGACTGTAGACTACTTGTAAAGATAAACAGATGTCACATTCATTTGGCCCCA	2089				
Qy	2024	ACATGGGTGAAAGTCGACCTACATTCGGCAAGGTGGCTTCAATGTCCTGATGGCCAAAG	2083				
Db	2090	ATATGGGAACTTAATCAACATATTCGACAACCTGGGTTATGACTCTGGCCAAA	2149				
Db	2084	TGGCTGTTGTCATGAGCAATGTCACATTCTATGTTGATTTTGCTC	2143				
Db	2150	TGCTGTTGTCATGAGTCAGTCACTGGCAAGTGTCCATCTAGGCC	2209				
Db	2144	GTGTTGGCCTGGAGATGGAGTGGAGTCTACTTTATGCAAGAGATGCTT	2203				
Db	2210	GAGTAGGGGGTCACTGAAATGAAAGAGTCACCTGCACTGGTAAATCTTGG	2269				
Qy	2204	AGACTCTGATCTGATCTTGTAAAGGGAGTACTGATGATCATGTTATGAGTTGG	2263				
Db	2270	AAACTGCTTCTTCTACCTGAGTCAACATGGCTTATCATGAAATCATTTGG	2329				
Qy	2324	TGAAAGAAATTAAAGCACCACATTGTTGCCACTCACTTCATGAGCTGACTGCTT	2383				
Db	2390	CAACAAAGTGTGCACTGAACTCTAGATGCTTGGCTTATTTGGACATTTG	2323				
Qy	2384	CAACAGAAATGGAGACAATGCAAAATGCTGGATAGCAATTTCATGTT	2443				
Db	2450	CAATCAG-----ATACCAACTGTTAATACTCATGTCATGAACTGCTT	2485				
Qy	2444	TGCAACATGCTGTTGCTTCAATGCAAGCTAACATGCTGTTACAGGTTCACCCAGGTG	2503				
Db	2486	CAGCACTCA----CCACTGAGACCTTAACTGTGTTATCAGGTGAGAAAGGTG	2539				
Qy	2504	CTTGTGATCAGAGTGTGTTGCTTCAATGCAAGCTAACATGCTGTTACCTGTT	2599				
Db	2564	TGGCTCTGGCTAGAAAAGGCATCGAAAGGATTCTGAGTTGGGATTTCCTCTTATGCCATTACATTTC	2623				
Qy	2600	TAGATGTRGCTTAAAGAAAGCCCTGGACATCTGGAGGATTCAGTATTTGGAGAAATCGC	2659				
Qy	2624	CAATGAAATTAAAGGGAGCTCAAACGGGAAAGAGAAATTTGA	2669				
Db	2660	AGGATATGATATCATGTAACCTGGCAAGAGTGTATCTGGAA	2705				
	RESULT 11						
US-10-109-791A-3							
	Sequence 3 , Application US/10109791A						
	Publication No. US20030138787A1						
	GENERAL INFORMATION:						
	APPLICANT: Biotech Oncologic Corp.						
	TITLE OF INVENTION: Functional Genetic Tests of DNA Mismatch Repair						
	FILE REFERENCE: B10L10_NP						
	CURRENT APPLICATION NUMBER: US/10/109-791A						
	CURRENT FILING DATE: 2002-09-06						
	NUMBER OF SEQ ID NOS: 315						
	SOFTWARE: Patentin version 3.1						
	SEQ ID NO 3						
	LENGTH: 2805						
	TYPE: DNA						
	ORGANISM: Homo sapiens						
	US-10-109-791A-3						
	Query Match	13.9%					
	Best Local Similarity	51.3%					
	Matches	1194					
	Conservative						
	Mismatches	1072					
	Indels	60					
	Gaps	7					
	Score	420.8					
	Pred. No.	B-8e-107;					
	Matched						
	359	ACTGGAGACTGTTAAAGTGGAACTGGAACTTGTGAAAGTTGAGGATATTCTGT	418				
	347	ATGGTATTGGCATATAAGGTCTCTCTGCAATCTCAGTGGACATCTCT	406				
	419	TGCTTAATAATGAAATGCAAATTCTCCGGTGAATTGGCTCTTGTCCCCTGTC	478				
	407	TGTTAACTATGATGTTGAGCTTCCATGGTGTGTTAAATGTCGGAGTTG	466				
	479	AGATGGATGTAAGTGGAGTTGGCTTGGCTTGGCTTGGCTTGGCTTAA	538				
	467	ATGGCCAGAGCAGGTGGATGGTGGATGGTGGATGGTGGATGGTGGAT	526				
	539	CGAAATTCTGATGATGAGCCACTTCACAAATTGGAGCTGCTTGTGTT	598				
	527	GGAAATTCCCTGATATAATGATCAGTGGCTCTCATCTGAGCTTGGAC	586				
	599	GGAGGAGATGCTTGTGACCGGGAGCTGGCAAAATCCAGTGAATACAGCC	658				
	587	CAGGGATGTTGTTTACGGGAGTGGCTTGTGAGTGGAGATGGCTTGTG	643				
	659	ATGCAATTCTGATGCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT	703				
	719	GAGATTGTGAGCTGGATGCTGGTGTGAGCTGTTGAGCTTGTGTT	766				
	704	ANGACATTATCTGGACCTTCACGGGTGTTGGCTTGGCTTGGCTTGG	763				
	767	CTGGTGGAGATTGGTGTGCTGGTTGGCTTGGCTTGGCTTGGCTTGG	826				
	764	GTGCTGATTGCGCAAAATGGAAATCAGGTTGCACTGTTGCGGTATCA	823				
	827	CTTATGGAGAACTTCTGGACCTTCACGGGTGTTGGCTTGGCTTGG	886				
	824	AGTTTGTAGAACTCTTCTGAGTATCCTGAGTTCACCTGAGTACTTGT	883				
	887	ACCTCAATAGTGTACATGGATGATGCTGCTGATGAGCTGTTGAGA	946				
	884	ACTTCAGCCAGTATGAACTGGTATGAGTGGCTTGGCTTGGCTTGG	943				
	947	GCACAAATCAGATGCTAAATGAAATGAAATGAAATGAAATGAAATGAA	1006				

Db	415	AATGGTATTGGCATAATAAGGCTTCTCCGGAAATCTCTCAGTTGAAGGACATTCTCT 474	Db	1486	CATTGAGCCATAATCTGTGATTAAGAGAAATAATGAAATGACTTGAAAAGAGATGC 1545
Qy	419	TTCGTTAATGAAATGAAATGAAATCTCCGGTGAATTCTCGCT 478	Qy	1484	ATATTTCGACAAACAACTGCCAATGTTCTCATCTTCACTTCTGAAAGTCACTTAAAC 1543
Db	475	TTCGTTAACATGATGATGTCAGGTTCCATGGTGTGGTAAATGTCGCAAGTG 534	Db	1546	AGTCACAACTTAAATAGTCAGGCCAGATGTCAGCTGGCAACAGATTAAAC 1605
Qy	479	AGATGGATGTTGAGTGGCTTAGGTATGTTATTAATCTAGAGTCCTGGTTAA 538	Qy	1544	TAGATAAAGGAAACAAATTGGACACGCTTCAGAATTACCAAGAAAGAACCAAAG 1603
Db	535	ATGCCAGAGAACGGTGGAGTGGCTGTTGGATTCAGAGAAACTAGGACTGT 594	Db	1606	TGATTTCCAGTGACAGTTGGTATTAATCTGTGAAACCTTAAGGATGGCTGAAATGGTCC 1665
Qy	539	CAGAATTCTAGATGATAACCCACTTCAGAAATTGGACTCTGGCTCTGGTT 598	Qy	1604	TCTGGAAACGCGCTAAATTCTCACTATGTTCTGAAACACTTAAGGATGGCTGAAATGGT 1663
Db	595	GTTGATTCCTGAAATGATGTCAGTCTCCAACTGGCTCTGTCATCCAGATGGAC 654	Db	1656	TTCGTTAACTAAATTTAGTACTGTGATATCCAGAAAGTATGGTTAAAT 1719
Qy	599	GCAGAGAATGTCCTGTTGATACCGGGAGACTGCAATCCAGTGAATCGGCTATGTTG 658	Qy	1664	TCACTTACAAACACTGAAACAAACTGAGATGAGATGAGATGAGATGAGATGAGATC 1723
Db	655	CAAGGGATGTTTACCGGAG---GAGAGACTGCTGGAAACATGGAGAC 711	Db	1720	TTACCAACAGCAATTGACTCTTTAAATGAAAGTACCAAAATAAAACGAAATATG 1779
Qy	659	ATGGAATATCTGATGCGGTGATGGTAACCTGAAAGAAACTGAAATTAAAGGA 718	Qy	1724	AAAGCTGTAGAGAAAGAAATTGGTAGCTCTGGTACTTCAGTGCAGTTCTCGGGG 1783
Db	712	AGATAATICAAGGGGAAATCTGATCACAGAAAGAAACTCTCCAA 771	Db	1780	AGAAAGCCAGGATGCGCTTGGTTAAAGBAATGTCATTTTCAGGCTATGTGAGC 1839
Qy	719	GAGATTCTGTCAGGATCTGGTAGGTCTGTAAGGGTTCA-----GTTGAGAC 766	Qy	1784	TGTTTGCGAGGTTAGTGGCTGGTACTCTGGTAGTGGTGTGACTGTTGGGATT 1843
Db	772	AGACATTATCAGACCTCAACGGTTGTTGAAAGGGAAAAGGAGACATGATA 831	Db	1840	CAATGCGAACACTCAATGTTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGC 1899
Qy	767	CTGTTGAGATTGCTCTGGCTTCAAGGGCTTGGGGTCACTTT 826	Qy	1844	TGGCTGCAGITGCCAACCTCCCTACACAAACAAATATCAGTCCACAGATAACGAG 1903
Db	832	GTGGTGTATTGGCGAAATGGAGATCAGTTCACTGCTGCGTAATCA 891	Db	1900	TGTCAAATGGAGACCTCTTCCATATGTAAGCAGCAAGGAA 1959
Qy	827	CTATGCGCAACTCTGGATGGACAACTATGGAAACTATACTCAAAATACA 886	Qy	1904	ATATTATCTGAAAGGGTAGGGCTAGGCTCTTGGCTGGAGACTCTAGATGGTTAACCTCA 1963
Db	892	AGTTTTGAACTCTTATCAGATGATTCCAACTTGGCAAGTGTACTTTG 951	Db	1960	GAATTATTTAAAGGATCATCCAGGCCATGCTTGGCTGGTGAATGAAATGCACTTA 2019
Qy	887	ACCTCAATAGTATCATGAGATTGATGATTCTGCTGTTGAACTATGGAGA 946	Qy	1964	TTCCTAAAGCTGAGCTGAGACTGTTAGGGAGAGAGTTGGTTGAGATTTCAAGGGCCCTA 2023
Db	952	ACTTCAGCCAGTATAATGAAATGAAATGGATATTGCAAGCTAACCTTTTCAAG 1011	Db	2020	TCTCTAAATGAGCTATACTTTGAAAGGATATAACGATGTTCCACATTTACTGGCCCA 2079
Qy	947	GCATACTGAGCTPAATAAAATTAGTGGCTTCTGTTGAACTGTGACTCT 1006	Qy	2024	ACATGGGTGGAAAGTCGACCTACATTGGCAGSCTTGGTAGTGTGCTGATGGCCAAAG 2083
Db	1012	GTTCGTTGAAATACCACTGGCTCTCTGGCTGCTGCTGCTGCTGCTG 1071	Db	2080	ATATGGGGGTATATCACATATTCACACAACTACTGGGTGATAGTACTCATGGCCAA 2139
Qy	1007	CTGGATGGTAAAGGTATTGCACTTGTGTTGAACTGTGAAATGTGAAAA 1066	Qy	2084	TRGGCTCTTTGGTCCATGTCACATGCTACATTCTGCTGTTGATTTTTCGTC 2143
Db	1072	CCCCCTCAAGGACAAAGACTTGTAAACCAGTGTGAACTCACTCTGAA 1131	Db	2140	TRGGCTGTTGGCTGGCACTGTCAGGAGTGTGTCATTTGGACTGCACTTGGC 2199
Qy	1067	AGATTAATCTGAGCTGATTAGTCAATCATCTGGTGAATGGCTGCGCTG 1126	Qy	2144	GTGTTGGCCTGAGATTGCGAGTGGCTTGTGTTGCTGTTGAGGTTCTACCTTATGCAAGGATGCTG 2203
Db	1132	GAATAGGGAGAGATTGAGTTAGTGGAGCTTGTAGAAATGCGAAATGGCGAGA 1191	Db	2200	GAGTAGGGCTGGCTGGCACTTGGCAATTGAAAGGAGTCTCCACGTTCATGGCTGAATGGTGG 2259
Qy	1127	ATTTGGCCACAT---CTGAAAGAAATTCTGAGATTGAGCTGAACTCTT 1183	Qy	2204	AGACTGGATCATGATCTGAAAGGAGTACTGATGAGATCATGGTGGATGGTTGG 2263
Db	1192	CTTACAGAAAGTTGAGTTTACTCTGGTGAATCTCAACCTGAACTT 1251	Db	2260	AAACTGTTCTCATCCCTGGCTGCAACAAAGATTCTATGAGTGAATTGG 2319
Qy	1184	AGGGAAAGAGCAGTTAGTGCACCTGTTGAAACTCTATCAGTCAGTACAGACTAC 1243	Qy	2264	GGCGTGGGACATCAACCTACGATGGCTTGTGTTGCTGTTGAGCACATGTG 2323
Db	1252	AAAGACAGGAGAAACTTACAGATTCTGAGAAATGGACTGATAATCAACTAC 1311	Db	2320	GRAGGAGAACTCTACCTACGATGGTTGAGTGGCTATGGCTATGAGATACTGTG 2379
Qy	1244	CATATATCAAAGTGTGGCTGATGTTGGCAATTGAAACTCTCATGGCT 1363	Qy	2384	CCACACAGAAATGGAGACATGGACATAAGAAATGGGGATAGAAATTTCATGTT 2443
Db	1372	TTTTGGTGTACTCTTCTACTGA-----TCTGTGTTGACTCTCCAGTTCA 1425	Db	2440	CCATACATG-----ATAACCAACTGTTAAATATCTACATGTC 2475
Qy	1364	TCTGGAAACACTCTGTTGACCTGATGAACTTGAAATGGGAAATACTGTTCTCTG 1423	Qy	2444	TTGCAACATGACCCCTCTAATCGGAAGCTAACATGCTTCAAGGTTACCCAGGTG 2503
Db	1426	TGATAGAAACAATTGATGATGAACTGGTAAACCTGTTGAAACCT 1485	Db	2476	CAGCAGTC-----CCAGTGAAGAGACCTAACATGCTTCAAGGTTACCCAGGTG 2529
Qy	1424	CATATGCCAAATTATCTGGCTCTGAAGGATGAGCAAGACATTGGCAAAATT 1483	Qy	2504	CTTGTGATCAGAGTTGGTATTCTGTGCTGAAATTGCAAAATTTCACCGAGTGTG 2563
Db	2530	TCTGTGATCAGAGTTGGATCTGAGCTTCAAGCTTAAGCATGTTAA 2589	Db	2530	TCTGTGATCAGAGTTGGATCTGAGCTTCAAGCTTAAGCATGTTAA 2589

RESULT 13

US-09-912-697-9

Sequence 9, Application US/09912697

GENERAL INFORMATION:

APPLICANT: Nicolaides, Nicholas C
Sass, Philip M
Grasso, Luigi M
APPLICANT: Kline, J Bradford
TITLE OF INVENTION: METHODS FOR GENERATING ANTIBIOTIC RESISTANT MICROBES AND
FILE REFERENCE: MOR-0040

CURRENT APPLICATION NUMBER: US/09/912,697

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 3145

TYPE: DNA

ORGANISM: Homo sapiens

US-09-912-697-9

	Query Match	Score	DB 10;	Length
Qy	Best Local Similarity	13.9%;	420	3145;
Db	Matches 1194;	Pred. No. 9.6e-107;	Indels 0;	Gaps 7;
Qy	359 ACTGGGACTCTGTAAGTAAAGTGAAACCCAGGGAAATTGGAAAGTTGAGATTTGAGATAATTCTGT	418		
Db	415 ATTGGATTTCGGCATTAAGGCTTCTCCTGGCAATTCTCTCAGTTGAGACATTCTCT	474		
Qy	419 TTGCCTPATAATGAAATGCAAATTCTCCGGTGAATTCTGCCTCTGGCTCCAAAACCTGGTC	478		
Db	475 TTGGTACAATGATAATGTCACCTCCATTGTTGTTAAATGTCGGTGTG	534		
Qy	479 AGAAATGGATCTGTAAGTTGGCTTAGCCATTGCTGATAATTCTAAGAGAGTCCTTGGCTTAA	538		
Db	535 ATGGCCAGAGAACGGTGGAGTTGGCTATGGATTCCATACAGAGAAACTTGGACTGT	594		
Qy	539 CAGAAATTCTGATGTTGCGGCTGATGGTAACTTGGAGCTGCTTGGCTCTGGTT	598		
Db	595 GTGGAATTCCCTGATATGATGATGTTCCAAATCTGGGCTCTCTCATCCAGATGGAC	654		
Qy	599 GCAGAGAAATGNCCTGTAACCGCGGAAACTGGCAATTCCAGTGAATAACGGCTATTTG	658		
Db	655 CAAAGGAAATGTTAACCGGAG--GAGGACTCTGGAGACATGGGAACCTGAGAC	711		
Qy	659 ATGCAATTCTGATGTCGGCTGATGGTAACTTGGAAAGAAAGAAACTGAAATTAAAGGGA	718		
Db	712 AGATAATTCAAAGGGGAAATTCTGATCACAGAAAGAAAAAGCTGACITTTCCACAA	771		
Qy	719 GAGATTGGTCAAGGATCTGGTCTGGTCAATGGCTGTOAAGGTTCA-----GTAAGAAC	766		
Db	772 AAGACATTATCAGGCTCAACCGTTGTTGAAAGGCCAAAAGGGAGGAGAATGAAATA	831		
Qy	767 CTGTTGCGAGTTGGTCTGGTCAATGGCTGCAATGGCTTGGGGTCATCTTT	826		
Db	832 GTGCTGTTGGCAGAATGGAGARTAGTTGCTGTTCACTGTCGGTGTATCA	891		
Qy	827 CTTATGCGAAACTACTGGGATGAGAGCAACTATGGAAACTATAGTCACACATACA	886		
Db	892 AGTTTGAACCTATCAGTGTCCAACTTGGACAGTTGGACTGACTTTGG	951		
Qy	887 ACCCTCATAGTGTACATGAGTAACTGAGTGTGCTGAGCTGAAATTTGAGGAA	946		

Qy	1484	ATAATTGCAAAACAACTGCOAATGATCCTGATCPATTGATAAGTCACTTAAC	1543	Oy	2564	TGGCTTGCTAGAGAAAGGCATCTGAGTTGGGATTTCCTCCATTGCCATAAATTC	2623		
Db	1546	ACTCAACATTAAATAGTCAGGAGATCTGGCTGGAACCTGGCAACAGATTAAC	1605	Db	2590	TAGAGTGTGCTAAGAGAACCTGGAACTGTGAGGAATTGCGATATGGAGATCGC	2649		
Qy	1544	TAGATAAGAAACACAAATTGGACAGCTCTGAAATTACCAAGAAAGAACCAAAG	1603	Oy	2624	CAAATGACATTAAGGGCAGCTTCAAAGGAAGAGAAATTGAA	2669		
Db	1606	TGGATTCCAGTCAGTGCACAGTTGGATATACTTCGTTGAACCTGTAAGAAC	1665	Db	2650	AAGGATATGATATGACAGCAAGCAAGCAACTGTPATCTGGA	2695		
Qy	1604	TGAGGAAGCAGCTAAATTCTCACTAATTGCTCAGAACCTGAGGGTAAAGT	1663	RESULT 15					
Db	1666	TTGTAA-----CAATAAAACCTTGTAGTCAGTGTGTTAAAT	1719	US-10-342-887-455					
Qy	1664	TGACCTATACAAAACCTCAAAACTGGAGATCACTGAGGAGTAAAGGTGATA	1723	Sequence 455, Application US/10342887					
Db	1720	TTACCAACAGGAAATTGACTCTTAAATGAGAGTATCCAGAAATGAGATATG	1779	Publication No. US20040058340A1					
Qy	1724	AAAGCTGTGAGTCAAAGGAAATTGGCTAGMCTGTTCTCCGGAGG	1783	GENERAL INFORMATION:					
Db	1780	AAAGAAGCCAGATGCCATTGCTAAGAATTGTCATATTCTTCAGGTATGAAAC	1839	APPLICANT: Dai, Hongye					
Qy	1784	TCTTTGAGGATAGCTGGTGTACCTGCTGTTGAGATGTTTCACTGAGTTGGGATT	1843	APPLICANT: He, Yudong					
Db	1840	CAATGAGACACTCATGATGTTGAGCTGAGCTGAGCTTGTGTCAG	1899	APPLICANT: Linsley, Peter S.					
Qy	1844	TGGCTGCCATTGCCAACTOCTCCTACACAAGACCAAATACTGTCACCGATAAGGAG	1903	APPLICANT: Mao, Mao					
Db	1900	TGTCAATGGACCTGTTCATATGTCACCCATTGGAAGAACAGAGGA	1959	APPLICANT: Roberts, Christopher J.					
Qy	1904	ATATTAATCTGAAGGCTGAGCTGATCAGATGGGTTAACTCCA	1963	APPLICANT: Van de Vlier, Laura Johanna					
Db	1960	GAATTATTAATAAAAGCATCCGGCATGCTTGTGAAAGTCAAGTGAATTGCA	2019	APPLICANT: Van de Vlier, Marc J.					
Qy	1964	TTCCTTAATGACTGTGAGCTACTTAAGGGAGAGGTGGTTCACTTCAAGCCCCTA	2023	APPLICANT: Bernards, Rene					
Db	2020	TTCCTTAATGACTGTGAGCTACTTAAGGGAGAGGTGGTTCACTTCAAGCCCCA	2079	TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients					
Qy	2024	ACATGGGTGGAAAGTCGACCTACATTCGGCAAGTGGCTCATTGCTGAGTCCCAG	2083	FILE REFERENCE: 93-01-188-999					
Db	2080	ATTAGGAGGTTCTATGCTACATTCTGCTACATTCTATGCTGTTGCTGAACTGGGTTGATCTGCTGAGTCCCAG	2139	CURRENT APPLICATION NUMBER: US/10/342, 887					
Qy	2084	TGGCTGTTCTATGCTACATTCTGCTACATTCTATGCTGTTGCTGAACTGGGTTGATCTGCTGAGTCCCAG	2143	CURRENT FILING DATE: 2003-01-15					
Db	2140	TGCGGTGTTGTCGGCATGTCAGTCAAGTGGCTGAGTCTCTAGCTTAGCCC	2199	PRIOR APPLICATION NUMBER: 60/298, 918					
Qy	2144	GTTGGGGCTGGGATGAGTGGGATGAGTGGGATGAGTGGGATGAGTGGT	2203	PRIOR FILING DATE: 2001-06-18					
Db	2200	GAGTAGGGCTGGGATGAGTGGGATGAGTGGGATGAGTGGGATGAGTGGT	2259	PRIOR APPLICATION NUMBER: 60/380, 710					
Qy	2204	AGACTGCATCTGAAAGGGCTACTGATAGCTGATATAATTGATGAGTGG	2263	PRIOR FILING DATE: 2002-05-14					
Db	2260	AACTGCTCTATCTGAAAGGAGCTTCTGAAAGGAGCTTCTGAAAGGAG	2319	PRIOR APPLICATION NUMBER: 10/172, 118					
Qy	2264	GCCCTGGGACATCAACCTGATGCTGCTTGGCTGGPATTGTCAGCTCATAG	2323	PRIOR FILING DATE: 2002-06-14					
Db	2320	GAAGGAGAACTCTGCTACCTGATGCTGATGCTGATGCTGATGCTG	2379	NUMBER OF SEQ ID NOS: 2695					
Qy	2324	TGCAAGAAATTAAAGCACCACATGTTGCAACCTGCTTCAAGCTCATAG	2383	SEQ ID NO: 455					
Db	2380	CAACAAAGATTGGCTTCTGCTTGTCAACCATTCTGAAACTCTGCTT	2439	LENGTH: 3145					
Qy	2384	CCACACAGAAATGGAGACAATGCAATAAGAAATGCTGGGATGCAAAATTTCATGTT	2443	TYPE: DNA					
Db	2440	CCACACAGAAATGGAGACAATGCAATAAGAAATGCTGGGATGCAAAATTTCATGTT	2475	ORGANISM: Homo sapiens					
Qy	2444	TGGCACACATTGACCCCTTAATGCAAGCTAACTATGCTTCACTGCTTCA	2503	US-10-342-887-455					
Db	2476	CAGGACTCA-----CCACTGAGAGACCTTAATCTGTTGAAAGGTG	2529	Query Match: 13.9% ; Score: 420.8 ; DB: 12 ; Pred. No. 9.6-1072 ; Mismatches: 0 ; Indels: 60 ; Gaps: 7 ; Matches: 1194; Conservative: 0 ; Prior filing date: 2003-01-15					
Qy	2504	CTTGTCATGAGTTGGCTTCTGCTTGTCACTGCTGAGCTGCTTCTGCTT	2589	TYPE: DNA					
Db	2530	TCTGTGATCAAGTGGATTTGGSATTCTGCTTGTCACTGCTGAGCTGCTT	2589	US-10-342-887-455					
Qy	767	CTGTTGAGATTGGCTCTGCTTGTCACTGCTGAGCTTCTGGGTCACTTT	826	Query Match: 13.9% ; Score: 420.8 ; DB: 12 ; Pred. No. 9.6-1072 ; Mismatches: 0 ; Indels: 60 ; Gaps: 7 ; Matches: 1194; Conservative: 0 ; Prior filing date: 2003-01-15					

832	GNGCTGATTGCCAGAAATGGGAATCAGGTGAGCTTCACTGTCGGTTAATCA	891	QY	1904	ATATTATACTTGAAAGCTGTAGGCATCCCTTGGAAGCTCAAGATGGGTTAACCTCCA	1963		
877	CTTATGCCAACTACTCTGGATGAGCAACTATGAAACCTATACAGTCACAAATACA	886	Db	1950	GAATTAAATTAAAAGCATCCAGGCACTGCTTGTAAAGTCAAGTAATGGCTTAA	2019		
892	ATTTTTGAACCTTATCAATGATTCAGTCACTTGCAGTTGACTGACTTTTG	951	QY	1964	TTCCTTAATGACTGTGAGCTAGTGTAGTTAGGGAGAGTGTGTTAGATATCACGGCCTA	2023		
887	ACCTCAATAGTTACATGAGATTAAGATCTGGCTATGAGGCCACTGAATTTATGAGA	946	Db	2020	TTCCTTAATGACCTATTTGAAAGATAAACAGATGTTCCACATTAATCTGGCCCCA	2079		
952	ACCTCGCCAGATPATAATGGATTTGGATTTTCAGG	1011	QY	2024	ACATGGGTGAAAGTCACCTACATGGAGGTGGTGAATGTCGATGTTGAACTGCTG	2083		
947	GCAATAGATGCTTAATAAATTAGTCTGTGCTATGAAAGTGTGACTG	1006	Db	2080	ATATGGGAGGTAAATCAACATATAATGAGAACACTGGGATATAGTCAACAA	2139		
1012	GTTCGTGTTGAGATACCATGCTCACTGCTCTGCTGTGCTGAAATAGTGTAAAA	1071	QY	2084	TTGGCTGTGTTGTTCCATGTGACAATGCTACATTCTATTCGTTGATTTGCTC	2143		
1007	CTGAAATGGGAAAGTGTAACTGATGTCAGTGGCTGTGAGCAACCTTACTAGATGTAAGAAG	1066	Db	2140	TGGGTGTTGCTGAGTCACTTATGCAAGAGATGCTGAGTCATGTCAGTCTAGGCC	2199		
1072	CCCCTCAAGGAAAGACTGTAACTGATGTCAGTGGCTCACTGATAAGAACAA	1131	QY	2144	GTGTTGCGCTGAGTGGCAAGCTGCGCTGAGGGAGTTCTACCTTTATGCAAGAGATGCTG	2203		
1067	AGATTAACCTGAGGCTGATTAGTGTCAATCATTCTGGAGATGTCGCTTCGCCAAG	1126	Db	2200	GAGTAGGCGCTGGTGTGAGTCAATGAAAGGTCACTGCTCACCTCTAGCTAAATSTGG	2259		
1132	GAATAGAGGAGATGATGAAATTAGTGGAAAGCTTGTAGAGATGAGAAATGECAGA	1191	QY	2204	AGACGTCATGATCTGAAAGGAGTCACTAGATCATCTGTTATATGATGCTGCTGG	2263		
1127	ATTGGAGGCCAT--CTGAAAAGAATTTCAGATATTGAGCGCTGACACACAACTCTG	1183	Db	2260	AAACTGCTCTTATCCCTGATCTGAACTCCAGGAAAGATCTPAATAATCATGATGATG	2319		
1192	CTTACAGAAGATTTACTCTGCTGATTCAGATCTAACGCACTTGTGCAAGTGTTC	1251	QY	2264	GCGTGTGAGCATCAACTTACATGGTTGGCTGAGCTGATGCTG	2323		
1184	ACAGGAAAGGCCAGTTAGTGCACCTGAACTCTATCACTGAGTACCAAGGTAC	1243	Db	2320	GAAGAGAACTCTACCTACATGGATTTGAGTGGCTGACTGCTAGTGCATAGT	2379		
1252	AAAGACAAGGCCAAACTTACAGATGTTACCGGACTCTATAGGTATATACTAC	1311	QY	2324	TTGAAAGAAUTTAAGGCCAACATTTGCTGCACTTCATGAGCTGATGCTAGT	2383		
1244	CATATATCAAAAGTGTGTTGGACCTGATGTTGGCAATTGCAACACTCTACAGTCAAGGGAAA	1303	Db	2380	CAACAAAGATGGTGTGCTGATGTTGCAACCTTACATGAACTTACATGACTACTGCTGG	2439		
1312	CTAATGTTATACGGCTCTGAAAAMCATGAGGAAAACACCGAAATTATGTTGGCAG	1371	QY	2384	CCAAACAGAATGGAGAACATTGAGCAATTGACATAAGAAATTCATGTT	2443		
1304	GTTATATTGATTCTCTGAGGAAATGGAGTGTGATAATCAGCTGAAATGTCATAGGTG	1363	Db	2440	CCAATCTG-----ATACATGTTAATATCTACATGTCATGTC	2475		
1372	TTTTTGTGACCTCTCTACTCTA-----TCTCGTGTCTGACTCTCTCAAGTTTCGGAAA	1425	QY	2444	TTGCACACATGACCCCTCTAATCSCAAGCTAATGCTTACAGGTTGACCCAGGTG	2503		
1364	TGTGAAACTCTGTTGACCTGTCACCTGAACTCTGAGATGGAAATACTTTCTCTG	1423	Db	2476	CAGCCTCA-----CCACTGAAAGGACCTTAACATGCTTATAGTCAAGAAGGTG	2529		
1426	TGATGAAACACTTGTGATGTTGAGTCACTGAGTGGAAAACCCTGTTAAACCTT	1485	QY	2504	CTTGTGTGAGGTTGGTATTCTGTTCTGGAATTGCAAAATTTCACCGAGTTGTTG	2563		
1424	CATATGACCCAAATTATTCGCTCTGAAAGTGTGAGCAACATGGAGCGRCAAAATT	1483	Db	2530	TCTGTGATCAAAAGTTGGATTCTGAGCTGAGTGGATTCTGAGCTGTAATTCTAACGATGAA	2589		
1486	CATTGATCTCAAATCTCAGTAAATTAGAATAATGAAATGACTCTGGAAAGATGC	1545	QY	2564	TGGCTCTGGCTGAGAAAAGGCATCTGACTTGGAGGATTCTCTATGCCATAATTC	2623		
1484	ATAATTGCAAAACCTCCAATGATCTGACTCTATTGATAAGTCACCTTAAAC	1543	Db	2590	TAGAGTGTGCTAAAGGAAAGCCCTGGACATCTGAGCTTACGTTGGAGATCGC	2649		
1546	AGTCACATATAAGTGACCCAGATCTGGCTTGGACCTGGCAACAGATTAAC	1605	QY	2624	CAAATGACATTAAGGAGGCTCAAAACGGAGAGAATTG	2669		
1544	TAGATAAGAACACACATTGACAGCTCTCAGTAAATTAGAATAATGAAAGAACCAAAG	1603	Db	2650	AAGGATATGATATCATGGAAACCAGCCTCAAAACGGAGAGAATTG	2695		
1604	TGAGGAGGACGACTAAATTCTCAGTAAATTGAGTATTACTCTCGTGAACCTGAAAGAAAGTCC	1665	QY	Search completed: April 9, 2004, 09:54:10 Job time : 1026 secs				
1666	TTCGTTAA----CATAAAACACTTGTGAGTCACTGAGTGTGTTAAAT	1719	Db					
1664	TACACCTATACTCAAACACTTAAACACTTGTGAGTGTGTTAAAT	1723	QY					
1720	TTACCAACAGAAATTGACTCTTAAATGAGATATAACAAATAAACAGATATG	1779	Db					
1724	AAAGCTGTCAGAAAGATTGCTAGCTGTTAGCTCAAGCTGGCTCCGAGTTCTCGGAGG	1783	QY					
1780	AGAAAGCCACAGTCATGCTTAAAGAAATTGTCATATTCTCAGGTTATGAGAC	1839	Db					
1784	TGTTGCGAGCTCTGAGTGTGTTACTGCTGTTGATGTTGCTGTTGGGATT	1843	QY					
1840	CAATGCGAGACCTCTCAATGATGTTAGCTGAGCTGTTGCTGTTGCTACG	1899	Db					
1844	TGGCTCCCASTTGCCCCAACCTCCCTACACAAAGACCAAATTAAGTCACGGAG	1903	QY					
1900	TGTCAAATGGACACCTGTCATATGTCACCGCATTITGGAAAGGACAGGAA	1959	Db					